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- GRAY SCALE DOCUMENTS

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Search completed: February
Job time: 29.8333 secs
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             Penn SG,
                                                                   hearts
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                                                                                                                                                                                                                                                 measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein #2449 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                                                                                                                                                                                         The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                 Claim 27; SEQ ID NO 28569; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                         ; Score 21; DB 22; Length 74;
; Pred. No. 4.2e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                      Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                     Penn SG, Hanzel DK, Chen W,
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
30-JAN-2001; 2001WO-US00669
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2000US-0236359
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                                                     03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
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19 SYDA 22
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
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Rank DR
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   Chen W,
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2: /cgn2_6/ptodata/1,

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      US-08-310-912A-126
US-09-301-085-126
US-09-301-085-126
PCT-US95-04589-126
US-08-557-006C-19
US-08-630-915A-184
US-08-630-915A-184
US-08-475-989-3
US-08-475-989-3
US-09-149-476-441
US-09-325-932A-181
US-09-325-932A-181
US-09-325-932A-177
US-09-325-932A-145
US-09-325-932A-145
US-09-318-793A-2
US-09-318-793A-2
US-09-318-793A-2
US-09-318-793A-2
US-09-318-793A-4
US-09-318-793A-4
US-09-318-793A-4
US-09-318-793A-4
US-09-318-793A-4
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US-08-565-349-1
US-08-682-643-4
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Sequence 126, App
Sequence 126, App
Sequence 127, Appl
Sequence 19, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 41, App
Sequence 11, Appl
Sequence 117, App
Sequence 117, App
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Sequence 2, Appli
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Sequence 46, Appli
Sequence 17, Appli
Sequence 46, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 5, Appli
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STREET: 225 Franklin St. CITY: Boston STATE: MA COUNTRY: USA ZIP: 02110-2904 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy dis COMPUTER: LBM PC COMPATEN: DEPARTING SYSTEM: PC-DO SOFTWARE: Patentin Rele CURRENT APPLICATION DATA: APPLICATION NUMBER: US- FILING DATE: September CLASSIFICATION UNDBER: US- FILING DATE: APPLICATION DATA: APPLICATION NUMBER: 08/ FILING DATE: APRIL 13, ATTORNEY/AGENT INFORMATION NAME: Lech, Karen F. FELECOMMUNICATION INFORMATION REGISTRATION UNDBER: 35 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION TELEPIONE: (617) 542-8906 TELEFAX: 100254 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7 amino acids TOPOLOGY: linear MOLECULE TYPE: protein	RESULT 1 US-08-310-912A-126 SEQUENCE 126, Applicat Patent No. 5981730 GENERAL INFORMATION: APPLICANT: AUSLIDE! APPLICANT: Staskaw APPLICANT: Dahlibec APPLICANT: Kunkel, APPLICANT: Kunkel, APPLICANT: Mindrin APPLICANT: Mindrin APPLICANT: My, Guo TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES CORRESPONDENCE ADDR	28 21 100 30 21 100 30 21 100 31 21 100 32 21 100 33 21 100 34 21 100 36 21 100 37 21 100 38 21 100 40 21 100 41 21 100 42 21 100 43 21 100 44 21 100 45 21 100
Franklin Street Floppy disk Floppy disk Ploppy disk Ploppy disk Ploppy disk PC compatible PC DOS/MS - DOS EENTIN Release #1.0 PTION DATA: US/08/310, 9 September 22, 1994 N: 536 NN DATA: NN DATA: NN DATA: NHEER: 08/227, 360 April 13, 1994 NIFORMATION: KAIFEN F: 35,238 KET NUMBER: 00786/ NI INFORMATION: 617) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906 7) 542-8906	icatic ON: DN: Dbel, skawia nckwia ncwia ncon ncon	319 3 US-08-682-643-3 0 341 4 US-09-134-001C-525 0 348 4 US-09-134-001C-474 0 376 4 US-09-134-001C-474 0 471 4 US-09-134-001C-425 0 442 2 US-08-414-938A-4 0 430 2 US-08-414-938A-4 0 452 2 US-08-472-172-6 0 455 2 US-08-472-172-2 0 459 2 US-08-472-172-2 0 459 2 US-08-472-172-2 0 459 2 US-08-472-172-2 0 1507 1 US-09-004-838-127 0 507 1 US-08-578-709-15 0 507 1 US-08-578-724A-22 0 509 3 US-08-58-78-22 0 509 545 4 US-09-066-46-3 0 545 4 US-09-066-40
. 3 OB	, PROBES, AND DETECTION	Sequence 3, Appli Sequence 5254, Ap Sequence 2, Appli Sequence 4742, Ap Sequence 4259, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 127, App Sequence 127, Appli Sequence 22, Appli Sequence 32, Appli Sequence 33, Appli Sequence 39, Appli Sequence 39, Appli Sequence 39, Appli Sequence 39, Appli Sequence 40, Appli

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SEQ ID NO 126
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CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 08/310,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES,
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Brent, Andrew F. APPLICANT: Dahlbeck, Douglas APPLICANT: Katagiri, Fumiaki
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EARLIER APPLICATION NUMBER: 08/227,360
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ausubel, Frederick MAPPLICANT: Staskawicz, Brian J.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                            NIPHILL OF INVENTION: 201
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
Fish & Richardson
Franklin Street Suite
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TITLE OF IN
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nes 4; Conservative (
                                                  COUNTRY: USA
ZIP: 02110-2904
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INVENTION: RPS2 GENE AND USES THEREOF
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Katagiri, Fumiaki
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Pred. No. 1.9e+05;
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SEQ ID NO 19
                                                                  Matches
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Patent No. 6258547
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PRIOR APPLICATION NUMBER: US 08/227,
APPLICATION NUMBER: US 08/227,
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
NAME: Clark Paul T.
ONTR
                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beri, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Forder, Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT FILING DATE: 1996-03-06
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB PRIOR FILING DATE: 1993-08-31
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1994-05-20
PRIOR APPLICATION NUMBER: GB
PRIOR FILING DATE: 1993-05-21
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 100254
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      ORGANISM: Rat
                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
 G
                                 1 SYDA 4
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SYDA
                                                                4;
                                                                                  Similarity
                                                                                                                                                                                                                                                                       PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 5; ilarity 100.0%; Pred No. 1.9e+05; Conservative 0; Mismatches 0;
                                                                  Conservative
                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                         GB 9310489,1
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                                                             0; Mismatches
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                                                                                Score 21;
Pred. No.
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                                                                                                DB 4; Length 14;
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RESULT 5

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US-08-930-605-15

: Sequence 15, Application US/08930605

: Patent No. 5981486
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                                                                                                                                                                                                                                                                                   RESULT 6
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Best Local Similarity 100.0%;
Matches 4; Conservative 0;
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                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 184:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                             STREET: 3000
                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                  FITLE OF INVENTION:
                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 03-APR-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                 COUNTRY: U.S.A. ZIP: 20007-5109
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                                                                                                  ADDRESSEE:
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                                                                               3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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ISHIKAWA, Yuji
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FOWLKES, Dana M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                FOLEY & LARDNER
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                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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δÃ RESULT 7 US-08-475-989-3 당 US-08-930-605-15 Best Loc Matches Sequence 3 Patent No. Query Match GENERAL INFORMATION: APPLICANT: CHONG, TELEFAX: (202) 672-5399 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,989
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,839
FILING DATE: 03-FEB-1993 COUNTRY: Canada
ZIP: M5G 1R7
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 TITLE OF INVENTION: Synthetic Haemophilus Influenzae TITLE OF INVENTION: Conjugate Vaccine NUMBER OF SEQUENCES: 56 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA: REFERENCE/DOCKET NUMBER: 05: TELECOMMUNICATION INFORMATION: APPLICATION NUMBER: PCT/C FILING DATE: 12-APR-1996 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: JP 7 FILING DATE: 13-APR-1995 PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS PRIOR APPLICATION DATA: APPLICANT: MOLECULE TYPE: STREET: Suite //
CITY: Toronto
STATE: Ontario APPLICANT: Local Similarity MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS NAME: Wegner, Harold C. REGISTRATION NUMBER: 25 10 SYDA 13 STRANDEDNESS CLASSIFICATION: CLASSIFICATION: TOPOLOGY: TELEPHONE: FILING DATE: 1 SYDA 4 APPLICATION NUMBER: ADDRESSEE: ENGTH: 25 amino acids , Application US/08475989 5679352 4; amino acid Suite 701, 330 University Avenue KANDIL, Ali SIA, Charles KLEIN, Michel 100.0%; Score 21; DB 2; Length 25; ilarity 100.0%; Pred. No. 55; Conservative 0; Mismatches 0; Indels linear Sim & McBurney (202)14-OCT-1997 , Pele 672-5300 JP 7-111033 Release #1.0, Version #1.30 PCT/JP96/01028 US/08/930,605 25,258 053466/0215 0 Gaps

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APPLICATION NUMBER:

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US-08-475-985-3
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                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA93/00041
FILING DATE: 03-FEB-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9202219.3
FILING DATE: 03-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CHONG, Pele
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CLASSIFICATION.
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
NAME: 24,973
                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,985
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,839
FILING DATE: 03-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Synthetic Haemophilus Influenzae
TITLE OF INVENTION: Conjugate Vaccine
NUMBER OF SEQUENCES: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 03-FEB-
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 100.0%; Score 21; DB 1; Length 35; Local Similarity 100.0%; Pred. No. 79; es 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toronto
: Ontario
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SIA, Charles
KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canada
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RESULT 9
US-08-472-172-15
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Matches 4; Conserv
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                                                                              TELEPHONE: (416) 595-
TELEFAX: (416) 595-11
TELEX: 063-24567 SIMB
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                           SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
                                                                                                                         NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,172
FILING DATE: 07-TUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/849,411
FILING DATE: 07-TUL-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
ZIP: M5G 1R6
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COPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sim & McBurney | Suite 701, 330 University Avenue
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(416) 59
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Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grass,
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Fahim, Raafat
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linear
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             single
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Query Match

100.0%; score 21;

DB 2;

Length 35;

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US-09-149-476-441

Sequence 441 Application US/09149476

Patent No. 6420526

GENERAL INFORMATION:
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Best Local
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            APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUTCATION INFORMATION:
TELEPHONE: (416) 595-1155
 EARLIER APPLICATION NUMBER: 60/040,162
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,839
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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ZIP: M5G 1R7
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STATE: Ontario
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KANDIL, Ali
SIA, Charles
KLEIN, Michel
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Suite 701, 330 University Avenue
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tive 0; Mismatches
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ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,502
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,633
ER FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R APPLICATION NUMBER: 60/047,583
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,617
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,618
R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,581

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,584

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,500

R FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/0.

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/0.

R FILING DATE: 1997-05-23
                                APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11
                                                                                                FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
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                                                                   APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11
                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,612
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
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PR FILING DATE: 1997-05-23

FR APPLICATION NUMBER: 60/047,586

FR FILING DATE: 1997-05-23

FR APPLICATION NUMBER: 60/047,590

FR FILING DATE: 1997-05-23

FR APPLICATION NUMBER: 60/047,594

FR FILING DATE: 1997-05-23

FR APPLICATION NUMBER: 60/047,594

FR APPLICATION NUMBER: 60/047,589
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IR FILLING DATE: 1997-08-22
IR APPLICATION NUMBER: 60/056,662
IR FILLING DATE: 1997-08-22
IR APPLICATION NUMBER: 60/056,872
IR FILLING DATE: 1997-08-22
                                                                                                                             APPLICATION NUMBER: 60/0
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/057,761
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-2
APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-2
APPLICATION NUMBER: 60/056,864
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,894
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,903
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APPLICATION NUMBER: 60/056,903
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APPLICATION NUMBER: 60/
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FILING DATE: 1997-08-22
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APPLICATION NUMBER:
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/0
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,877
FILING DATE: 1997-08-22
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/043,672
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RESULT 12
US-09-034-916-11
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Best Local S
Matches 4
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Patent No. 60463]
                                                                                                                                            GENERAL INFORMATION:

APPLICANT: GEBE, JOHN A.

APPLICANT: SIDAK, ANTHONY W.

APPLICANT: ARUFFO, ALEJANDRO A.

TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR

TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLY

TITLE OF INVENTION: ANTHODIES THERETO

NUMBER OF SEQUENCES: 17
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COMPUTER READABLE FORM:
                                                                                                                          CORRESPONDENCE ADDRESS
                                                     CITY: MENLO PARK
STATE: CALIFORNIA
                                                                        ADDRESSEE: ROBLING ADDRESSEE: ROBLING GUREET: 90 MIDDLEFIELD
                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                           35 SYDA
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ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,875
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,862
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,987
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,908
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/048,964
ER FILING DATE: 1997-06-06
ER FILING DATE: 1997-06-06
ER FILING DATE: 1997-06-06
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ER APPLICATION NUMBER: 60/047,593
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,614
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/043,578
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER APPLICATION NUMBER: 60/043,576
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ER FILING DATE: 1997-05-23
GR APPLICATION NUMBER: 60/043,670
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/056,632
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,884
APPLICATION NUMBER: 60/056,884
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APPLICATION NUMBER: 60/057,669
FILING DATE: 1997-09-05
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FILING DATE: 1997-06-13
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-08-22
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NUMBER: 60/047,593
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                                                                                  & ASSOCIATES |
FIELD ROAD, SUITE
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Gaps

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SOFTWARE: FastSEQ for Win SEQ ID NO 181
LENGTH: 132
TYPE: PRT
ORGANISM: Pinus radiata
US-09-325-932A-181
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Best Local Similarity
A; Conserv
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                                                                                                      US-09-325-932A-177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Filnn, Barry
APPLICANT: Lasham, Annette
APPLICANT: Losham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant devel
                                                    Sequence 177, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 181, Application US/09325932A Patent No. 6451604
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
   APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 325-782
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 5998-0020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60 FILING DATE: 06-MAR-1997 ATTORNEY/AGENT INFORMATION: NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                             126 SYDA 129
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COMPUTER: II
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Compositions affecting programmed cell
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GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
FITTLE OF INVENTION: Compositions affecting F
TITLE OF INVENTION: death and their use in t
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 145
LENGTH: 204
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 275
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US-09-615-192A-275
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US-09-325-932A-145
; Sequence 145, Application US/09325932A
; Patent No. 6451604
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 177
LENGTH: 133
TYPE: PRT
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APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin (
FILE REFERENCE: 11000.1003c4U
CURRENT FILING DATE: 2000-07-12
DRIOR APPLICATION NUMBER: US 08/975,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: FILE REFERENCE: 1022
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                  Compositions affecting programmed cell death and their use in the modification
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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Pred. No.
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                                                                                                                                                  of forestry plant
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US-09-286-690-2

; Sequence 2, Application US/09286690

; Patent No. 6103511
                                                                                                  RESULT 18
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US-08-578-709-11
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GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/578,709
FILING DATE: 28-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/00838
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 114316/1994
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gubtisky Ionis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Applicat Patent No. 5814509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: GUDINSKY, LOUIS
REGISTRATION NUMBER: 24,835
REFERENCE/DOCKET NUMBER: Q4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TANABE, Tadashi
TITLE OF INVENTION: PROSTA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                               82 SYDA 85
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                              1 SYDA 4
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21 SYDA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SUGHRUE, MION, ZINN, MACPEA
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100 les 4; Conservative
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100.0%; F
tive 0;
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Pred. No. 5.9e+02;
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Pred. No.
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RESULT 20
US-09-318-793A-4
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SOFTWARE: Pac
SOFTWARE: Pac
SEQ ID NO 4
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; SEQ ID NO 2
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Orpinomyces sp. PC-2
US-09-286-690-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-318-794A-2
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LENGTH: 271
TYPE: PRT
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Sequence 4, Application US/09318793A Patent No. 6184007
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GENERAL INFORMATION:
                                                                                                        APPLICANT: Dusch, Nicole
APPLICANT: Kalinowski, Jorn
APPLICANT: Kalinowski, Jorn
APPLICANT: Publer, Alfred
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID BY ENHANCEMENT OF THE PAND GENE IN MICROORGANISMS
FILE REFERENCE: 21123/260204
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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Matches
                                                            CURRENT APPLICATION NUMBER: US/09/318/793A
CURRENT FILING DATE: 1999-05-26
NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DEGUSSA AKTIENGESELLSCHAFT
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID USING CORVIEFORM BACTERIA
FILE REFERENCE: eggeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04.05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
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TITLE OF INVENTION: Lichenase and Coding Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 55-96
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                                                                                                                                                                                                                                                                                                                                                                                  31 SYDA 34
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                                             PatentIn Ver. 2.1
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Pred., No. 6.8e+02;
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Pred: No. 6.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 271;
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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5603
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US-08-936-165A-462
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SEQ ID NO 5603
LENGTH: 287
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5603, Applic Patent No. 6380370 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,764
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No. 6348582
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                   TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides TITLE OF INVENTION: Polypeptides and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                        STREET: 709 Swedeland CITY: King of Prussia
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                                                                          COUNTRY:
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                                                                                               PΑ
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Rosenberg, Martin
Ward, Judith
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                                                                          USA
                                                                                                                                                                                                                                                                                                                                  Knowles, David
Lonetto, Michael
                                                                                                                                                                                                                                                                                                Pratt, Julie
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                                                                                                                                                                                                                                                                                                                                                                                       Burnham, Martin
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                                                                                                                                                                                                                                                                                                                                                                                                            Black, Michael
: Diskette
IBM Compatible
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pred. No. 7.2e+02;
pred. no. 7.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 23
US-08-038-932B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi PA-1-2-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
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                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4
FILING DATE: 08-JUN-1992
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                    STREET: 110
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REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                      STATE: Washington, D.C. COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SYDA 4
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           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 100.0%; Score 21; I Local Similarity 100.0%; Pred. No. 7 Local Similarity 00.0%; Mismatches 4; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08038932B
                                                                                                                                                                                                                                                                                                        1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoneya, Takashi
Miyake, Toshio
Aoyama, Atsuo
                                                                                                                                                                                                                                                                                                                                                                                     Wada, Akiyoshi
                                                                                                                                                                                                                                                                                                                                                                                                 Endo, Kimiko
                                                                                                                                                                                                                                                                                                                                                                                                                     Kidokoro, Shun-ichi
Miki, Yoichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kai, Ken-ichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagao, Hiromasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss: single
linear
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14-AUG-1992
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             JP 4-237606
                                                                                                                           US/08/038,932B
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RESULT 25
US-08-682-643-4
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                                                                                                                                                                            Sequence 4, Application US/08682643 Patent No. 6103512 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acid
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TELEX: 248453
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2" 1.44 mb Floppy diskette
COMPUTER: IBM 486/DX100 ValuePoint PC
                                                                                                            APPLICANT: Venema, Gerhardus; Eijsink, Vincentius
TITLE OF INVENTION: Thermostable Variants of Neutral
TITLE OF INVENTION: Proteases of Bacillus Stearothermophilus and
NITHER OF INVENTION: Bacillus Thermoproteolyticus
                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                   OPERATING SYSTEM: Microsoft OPERATING SYSTEM: Version 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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        PatentIn
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100.0%; Pr
0;
                                Microsoft Windows NT Workstation
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100.0%; Pred. No. 8e+02;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                Score 21;
Pred. No.
#1.0 Version #1.30 (EPO),
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TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908)530-6584
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
                                                                                                                                                                      COMPUTER: IBM COMPATIB
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for
CURRENT APPLICATION DATA:
                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                               ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CAROL
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 52
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: No. 63037
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Deussen, Heinz-Josef
APPLICANT: Roggen, Erwin Ludo
TITLE OF INVENTION: A Modified NUMBER OF SECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Olsen, Arne Agerlin
APPLICANT: Fatum, Tine Muxoll
APPLICANT: Deussen, Heinz-Josef
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FILING DATE: 27-JAN J.
ATTORNEY/AGENT INFORMATION:
NAME: Michaelson, Peter L.
NAME: Michaelson, Peter L.
30090
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REFERENCE/DOCKET NUMBER: RI
TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                       CITY:
STATE:
                                                                                                                                                                                                                                                                          ZIP:
                            TELEPHONE:
                                                                                                                                              APPLICATION NUMBER: FILING DATE: 25-JUN
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                                                                                                                            CLASSIFICATION:
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STRANDEDNESS: unl
TOPOLOGY: unknow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SYDA 4
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                                                                                                                                                                                                                                                                                                                      New York
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                  212-878-9655
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                                                                                                                                                                                                                                           Diskette
                                                                                                                               25-JUN-1998
4: 435
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                                                            5256.200<sub>1</sub>-us
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; STRAIN: Bacillus Thermoproteolyticus
US-09-104-623A-5
                                                                                                                                                                                                                                                                                                                      RESULT 28
US-08-682-643-3
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EARLIER FILING DATE: 1998-01-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 316
TYPE: PRT
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Matches
                                                                                                                                                                                                                                                             Sequence 3, Application US/08682643 Patent No. 6103512 GENERAL INFORMATION:
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APPLICANT: Olsen, Arne Agerlin
APPLICANT: Prent , Annette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A Modified Enzyme for Skin Care FILE REFERENCE: 4922.204-US CURRENT APPLICATION NUMBER: US/09/019,532B CURRENT FILING DATE: 1998-02-05 EARLIER APPLICATION NUMBER: 0038/97 EARLIER FILING DATE: 1997-01-10 EARLIER APPLICATION NUMBER: 0754/97 EARLIER FILING DATE: 1997-06-25 EARLIER APPLICATION NUMBER: 0754/97 EARLIER FILING DATE: 1997-07-07
                                                              NUMBER OF SEVEN.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2" 1.44 Mb Floppy diskette

COMPUTER: IBM 486/DX100 ValueFoint PC

COMPUTER: IBM 486/DX100 ValueFoint PC

COMPUTER: Microsoft Windows NT Workstation
         SOFTWARE: PatentIn Release #1.0 Versu SOFTWARE: and Windows No. 6103512epad CURRENT APPLICATION DATA:
                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                65 SYDA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                   Venema, Gerhardus; Eijsink, Vincentius
VENTION: Thermostable Variants of Neutral
VENTION: Proteases of Bacillus Stearothermophilus and
VENTION: Bacillus Thermoproteolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                      PatentIn Release #1.0 Version #1.30 (EPO),
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1997-07-07
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100.0%; P
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US/08/682,643
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Pred. No.
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Pred. No. 8e+02;
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8e+02;
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RESULT 30
US-09-147-236-2
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5254
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US-09-134-001C-5254
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Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
DEFICE ADDITCATON NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5254
                                                               GENERAL INFORMATION:
                                                                               Sequence 2, Application US/09147236A Patent No. 6316251
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Best Local Similarity
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APPLICANT: TONOUCHI, Naoto
APPLICANT: TSUCHIDA, Takayasu
APPLICANT: YOSHINAGA, Fumihiro
APPLICANT: TAHARA, Naoki
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
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FILING DATE: 27-JAN-94
ATTORNEY/AGENT INFORMATION:
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HYPOTHETICAL:
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                                                                                                                                                                                 265 SYDA 268
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REGISTRATION NUMBER: 30090
REFERENCE/DOCKET NUMBER: 1
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STRANDEDNESS: unl
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Pred. No.
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Pred. No. 8.4e+02;
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RESULT 32
US-09-134-001C-4259
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US-09-147-236-2
                          GENERAL INFORMATION:
APPLICANT: LYND DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
FILE REFERENCE: GTC-007
CURRENT ELLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR TILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
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APPLICANT: LYND DOUCETTE-Stamm et al
APPLICANT: LYND DOUCETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PELING DATE: 1997-10-05
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER DE GEO TO NO. 1671-14
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LENGTH: 348
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LENGTH: 341
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EARLIER APPLICATION NUMBER: PCT/JP97/03633
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Acetobacter xylinum
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les 4; Conserv
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                     FILING DATE: 1997-08-14
ID NOS: 5674
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Pred. No.
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US-08-414-938A-4
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US-09-465-558-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: Microsoft O
SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08414938A Patent No. 5994627
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Best Local S
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LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 70, Application US/09465558 Patent No. 6436657
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                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LAGUDAH,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MOTAKINYO, LAYO O.
APPLICANT: OTOZGO JT, EMIL M.
TITLE OF INVENTION: TETRAHYDROFOLATE METABOLIC ENZYMES
FILE REFERENCE: BB1322 US NA
CURRENT APPLICATION NUMBER: US/09/465,558
CURRENT FILING DATE: 1999-12-17
EARLIER APPLICATION NUMBER: 60/112,734
EARLIER FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/414,938 FILLING DATE: March 31, 1995 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 SYDA 385
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REGISTRATION NUMBER:
                                                                                                                                                                                         ZIP: 10036
                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                      CITY: NEW YORK
                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                       ADDRESSEE:
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                JOHN P.
                                                                                                                                                                                                                         NEW YORK
                                                                                                                                                                                                                                                     E: COOPER & DUNHAM
1185 AVENUE OF THE
                                                                                                                                                                                                       UNITED STATES OF AMERICA
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GENETIC SEQUENCES CONFERRING
NEMATODE RESISTANCE IN PLANTS
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Pred. No. 1e+03;
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                                                                                                          Version #1.25
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; STRANDEDNESS: not rel
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-945-848-8
RESULT 36
US-08-472-172-6
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                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cawley, Jr, Thomas A.
REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 1903
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08945848 Patent No. 5968772 GENERAL INFORMATION:
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                       Matches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: + 212 278 0400
TELEFAX: + 212 391 0525
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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293 SYDA 296
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   71 SYDA 74
                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606
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                                                                                                                                                                                                                                                                                        LENGTH:
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: United States of America
                                                                                                                                                                                                                                                                                        430 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATSUSHIRO, Aizo
VENTION: PEARL PROTEIN(NACREIN) AND PROCESS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marshall, O'Toole, Gerstein, Murray & Borun 3 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                      not relevant
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100.0%; Pred. No. 1.1e+03;
htive 0; Mismatches 0;
                                                                                                                                                   100.0%; Score 21; DB 2; 100.0%; Pred. No. 1.1e+03;
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                                                                                                                                                                     Length 430;
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Best Local Similarity
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US-08-472-172-6
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                                                                                                                                                               Sequence 4, Application US/08472172 Patent No. 5985288 GENERAL INFORMATION:
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APPLICANT: Munson
APPLICANT: Grass,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 063-24567 SIMBAS INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
TELEPHONE: (416) 595-1163
                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION UDABER: US 07/849,411
FILING DATE: 07-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,172
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Klein, Michel
TITLE OF INVENTION: Outer Membrane Protein Pl and Peptides
TITLE OF INVENTION: of Haemophilus Influenzae Type B
                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                    144 SYDA 147
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STRANDEDNESS: sir
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                                              Chong, Pele Y Y
Fahim, Raafat
Sia, Charles D Y
McVerry, Patrick
Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suite 701,
                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 2; ilarity 100.0%; Pred. No. 1.1e+03; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McVerry, Patrick
Klein, Michel
                                                                                                                                                  Munson,
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                                                                                                                                   Grass, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fahim, Raafat
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Outer Membrane Protein Pl and Peptides of Haemophilus Influenzae Type B 26
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                                                                                                                                                    Robert
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FILING DALL.

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/849,411
FILING DATE: 07-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-471
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-472-172-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-1163
TELEX: 063-24567 SIMBAS
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,172
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                 TITLE OF INVENTION: Outer Membrane Protein Pl
TITLE OF INVENTION: of Haemophilus Influenzae
NUMBER OF SEQUENCES: 26
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                                                                                                       COUNTRY:
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ZIP: M5G 1R6
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STRANDEDNESS: sir
                                                                                                                                                                                ADDRESSEE:
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                                                                                        MSG 1R6
                                                                                                                                             Toronto
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                                                                                                                           Untario
                                                                                                                                                     JE: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                   Sia, Charles D Y
McVerry, Patrick
Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                         Chong, Pele Y Y
Fahim, Raafat
                                                                                                                                                                                                                                                                                                                                                             Grass,
                                                                                                                                                                                                                                                                                                                                                                          Munson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                              Jr., Robert S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 2; 100.0%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                       FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: EINHOCK, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/849,411
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: US,
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Michelmore, Richard W. APPLICANT: Shen, Kathy APPLICANT: Meyers, Blake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 SYDA 151
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, | Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Embarcac
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 595-1163
TELEX: 063-24567 SIMBAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0:
FILING DATE: 07-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127, Application US/09004838
5. 6350933
                                                                                                                                                                                                                                                                                                                                                                                                                            94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 2; illarity 100.0%; Pred: No. 1.2e+03; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (416) 595-1155
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                                                                                                                                                                                                                                                                                  US/09/004,838
                                                                                                      023070-078810US
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-578-709-15
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Matches
                                                                                        Query Match
                                                             Matches
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                                                                                                                                                                                              TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: Q4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/JP95/00838
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,709
FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/JP95/00838
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 114316/1994
FILING DATE: 28-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Gubinsky, Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 SYDA 147
                                                                                                                                                                     TYPE: a
                                                                          Local Similarity
 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..487
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                              1 SYDA 4
SYDA 85
                                                          4;
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                                                                                                                                                                  amino acid
                                                                                                                                                                                 500 amino acids
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                                                            Conservative
                                                                                                                                                                                                                            (202)293-7860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                         100.0%; S
100.0%; P
ative 0;
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100.0%; P
ative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tadashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "RG2T deduced sequence"
                                                                                                                                                                                                                                                                                       24,835
                                                                                                                                                                                                                                                                            Q40439
                                                       Score 21; DB 2;
Pred. No. 1.3e+03;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 4;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                     Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 487;
                                                          Indels
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                                                          0,
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                                                          Gaps
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RESULT 41

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                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-457-274A-22
                                                                                                                                                                                  Sequence 22, Application PC/TUS9505758 GENERAL INFORMATION:
APPLICANT: Cornell Research Founda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/08457274A Patent No. 5734086
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                POSITION IN GENOME: Chromosome 5
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Scott, Jeffrey APPLICANT: Tomita, Takashi TITLE OF INVENTION: Cytoch
                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                  348 SYDA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Musca domestica STRAIN: Rutgers DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: /10 - 1600 - 716-263-1600 - 716-263-1600
                                                STATE:
                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rochester STATE: New York
                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                 1 SYDA 4
                                    T: P.O. Box 1051, Clinton Square Rochester : New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldman, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Nixon, Hargrave, Devans & Doyle P.O. Box 1051, Clinton Square
                                                                                                                                                                 Cornell Research Foundation, Inc. VENTION: Cytochrome P450lpr Gene and Its
                                USA
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                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 1; 100.0%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/457,274A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19603/240 (D-1519)
                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                 Devans & Doyle
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Length 507;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                              Gaps
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polon-"

MEDIUM TYPE: COMPUTER: II

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RESULT 43
US-08-822-324-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity luu.
Thes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08822324
Patent No. 6129917
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Travis, James
APPLICANT: Genco, Caroline A.
TITLE OF INVENTION: IMMUNGENIC
TITLE OF INVENTION: PORPHYROMOI
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
FILING DALL.

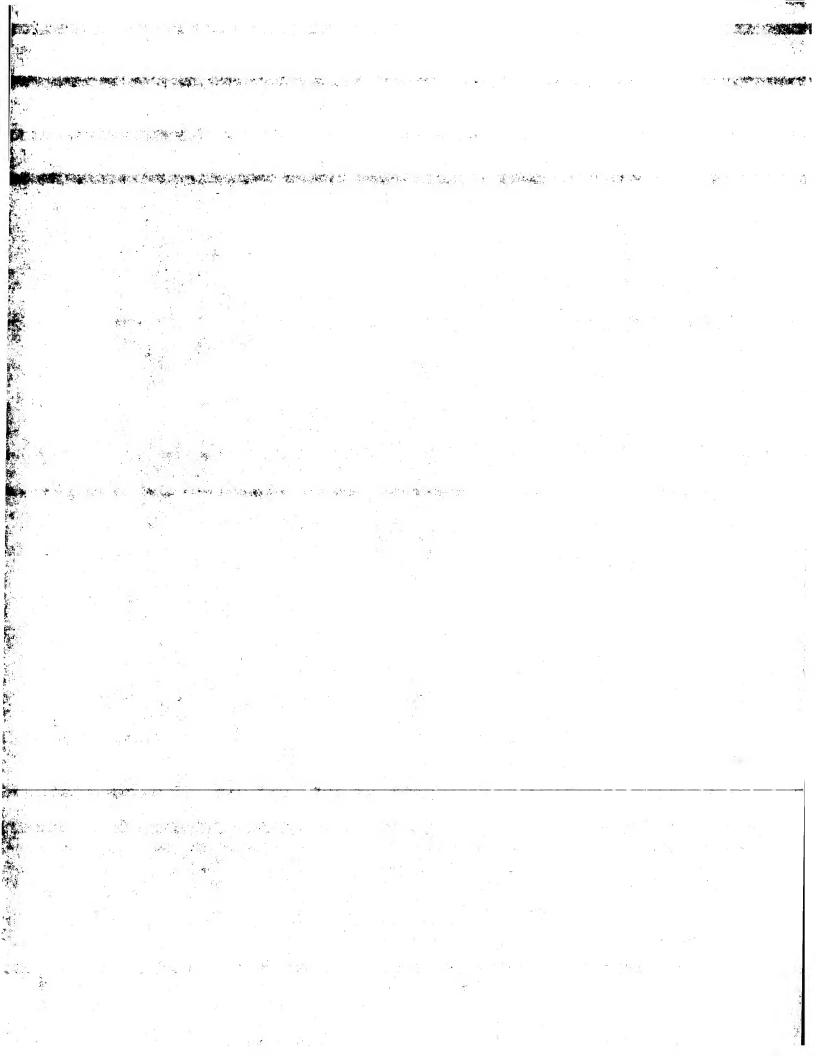
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,945
APPLICATION NUMBER: 22-MAR-1996
APPLICATION NUMBER: 22-MAR-1996
                                                                                    COMPUTER: IBM FC compatible
COMPUTER: FIRM FC COMPATER
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,324
FILING DATE: 21-MAR-1997
FILING DATE: 21-MAR-1997
                                                                                                                                                                                                            COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: pr
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 5
                                                                                                                                                                                                                                                                                           STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: GOJGMAN, MICHAEL L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 SYDA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Greenlee, Winner and Sullivan, p.C. STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN: Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goldman, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potempa, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Musca domestica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                        IMMUNOGENIC COMPOSITIONS COMPRISING PEPTIDES AND PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 5; I 100.0%; Pred. No. 1.3e+03; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US95/05758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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US-09-066-046-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вр
Query Match
Best Local Similarity 100.
Thes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-822-324-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 488-8080
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                          TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 111
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 SYDA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ferber, Donna M. REGISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                               NAME: Superko, Colleen
REGISTRATION NUMBER: 39,850
REFERENCE/DOCKET NUMBER: 100
TELECOMMUNICATION INFORMATION: |
TELEPHONE: (617) 526-6000
                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/066,046A
FILING DATE: 24-Apr-1998 |
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Superko, Colleen
                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk |
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release | #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CHARACTERIZATION OF GRANULOCYTIC EHRLICHIA AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MURPHY, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09066046A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STOREY, James
BELTZ, Gerald A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUGHLIN, Richard T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States
                         100.0%; Score 21; DB 4;
100.0%; Pred. No. 1.4e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 3;
Pred. No. 1.3e+03;
; Mismatches 0;
                                                                                                                                                                                                                                                                                         106.941.155
                                                           Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 509;
                           Indels
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                           0;
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                         Gaps
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                         0;
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RESULT 45
US-08-557-006C-40
Sequence 40, Application US/08557006C
Sequence 40, Application US/08557006C
GENERAL INFORMATION:
APPLICANT: Beri, Rajindar K.
APPLICANT: Beri, Rajindar K.
APPLICANT: Beri, Rajindar K.
APPLICANT: Berider, Robert A.
APPLICANT: Berider, Robert A.
APPLICANT: Border, Robert A.
APPLICANTON UNMER: GB 9310499.1
APPLICANTON UNMER: GB 9310499.1
APPLICANTON UNMER: GB 9310010.7
APPLICANTON UNMER: GB 9310010.7
APPLICANTON ROBER: BORDER, ROBERT A.
APPLICANTON UNMER: GB 9310010.7
APPLICANTON ROBER: BORDER, ROBERT A.
APPLICANTON ROBERT A.
APPLICATION ROBERT A.
APPLICANTON ROBERT A.
APPLICANTON ROBERT A.
APPLICATION ROBERT A.
APPLICANTON ROBERT A.
APPLICATION ROBERT A.
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
         129505 seqs, 22169297 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   February
                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA: *
// cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *
                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.3 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, 2003, 11:22:09; Search time 5.83333 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapext 0.5
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15.202 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

16 21 1 17 21 1																		No. Score M
100.0	0.0	0.0	00.0	00.0	00.0	00.0	00.0	00.0	00.0	00.0	00.0	00.0	00.0	00.0	00.0	00.0	100.0	Match Length
175 219	175	175	144	140	140	140	140	124	114	74	74	74	65	65	65	22	7	igth DB
99	9 0	6	10	10	10	10	10	9	10	10	10	10	10	10	10	10	10	
US-09-738-626-6309 US-09-738-626-5341	US-09-738-626-6300	US=U9+864-/61-39939	US-09-881-752A-306	US-09-970-088-14	US-09-970-088-13	US-09-970-088-12	US-09-970-088-11	US-09-796-692-1351	US-09-864-761-45709	US-09-864-761-47595	US-09-864-761-42544	US-09-864-761-35748	US-09-864-761-39908	US-09-864-761-34172	US-09-864-761-34093	US-09-879-957-184	US-09-867-852-126	ID
Sequence 5341. Ap		sequence 39939, A	306,	Sequence 14, Appl	13,	12,	Sequence 11, Appl	\mathbf{r}		Sequence 47595, A	Sequence 42544, A	Sequence 35748, A	Sequence 39908, A	Sequence 34172, A	Sequence 34093, A	Sequence 184, App	Sequence 126, App	Description

RESULT 2

0;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
552	549	506	506	491	439	416	378	360	360	359	352	352	345	343	339	332	332	321	290	271	267	267	267	256	248
10	10	10	10	10	10	9	9	10	9	10	10	9	9	10	10	10	9	9	10	9	9	9	9	9	10
US-09-824-735-4	US-09-925-302-477	US-09-815-242-11757	US-09-815-242-5045	US-09-820-893-56	US-09-815-242-5696	US-09-971-536-60	US-09-738-626-5738	US-09-815-242-11378	US-09-738-626-5241	US-09-799-777-45	US-09-888-615-95	US-09-808-602-105	US-09-738-626-4252	US-09-815-242-10844	US-09-815-242-10953	US-09-962-618-2	US-09-738-626-4308	US-09-808-602-106	US-09-939-980-462	US-09-738-626-3633	US-09-808-602-101	US-09-808-602-25	US-09-808-602-23	US-09-993-308-2	US-09-925-299-958
Sequence 4, Appli	Sequence 477, App	Sequence 11757, A	Sequence 5045, Ap	Sequence 56, Appl	Sequence 5696, Ap	Sequence 60, Appl	Sequence 5738, Ap	Sequence 11378, A		Sequence 45, Appl	Sequence 95, Appl	Sequence 105, App	Sequence 4252, Ap	Sequence 10844, A	Sequence 10953, A	Sequence 2, Appli	Sequence 4308, Ap	Sequence 106, App	Sequence 462, App	Sequence 3633, Ap	Sequence 101, App		23	Sequence 2, Appli	Sequence 958, App

ALIGNMENTS

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Вþ
                                       QΥ
                                                                                                                                                                    ; ORGANISM: Arabidopsis thaliana US-09-867-852-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-867-852-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 126, Application US/09867852
; Patent No. US20020147324A1
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/867,852
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
                                                                                                     Query Match
Best Local Similarity
                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: DETECTION METHODS
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                         1 SYDA 4
  SYDA
                                                                                   4;
    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunkel, Barbara N.
Mindrinos, Michael N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dahlbeck, Douglas
Katagiri, Fumiaki
                                                                                   Conservative
                                                                                                  100.0%;
                                                                                   0;
                                                                                 Score 21; DB 10;
Pred. No. 1.1e+05;
; Mismatches 0;
                                                                                                                      Length 7;
                                                                                   Indels
                                                                                   0,
                                                                                   Gaps
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RESULT 3
US-09-864-761-34093
; Sequence 34093, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                         1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
WATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN_OF_INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/630,915 FILING DATE: 03-APR-1996
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
ULE TYPE: peptide
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FOWLKES, Dana
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                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB Pred. No. 27; Mismatches
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US-09-864-761-34172
; Sequence 34172, Application US/09864761
; Patent No. US20020048763A1
    GENERAL INFORMATION:
APPLICANT: Penn, Sh
APPLICANT: Rank, D
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Best Local :
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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Penn, Sharron G
Rank, David R.
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                      NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

NN: EXPRESSED IN HEART, SIGNAL = 2.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 2.8

NN: EXPRESSED IN HELA, SIGNAL = 1.1

NN: EXPRESSED IN HELA, SIGNAL = 1.1

NN: EXPRESSED IN HELA, SIGNAL = 1.9

NN: EXPRESSED IN HBL10O, SIGNAL = 1.4

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

NN: EXPRESSED IN LIVER, SIGNAL = 1.4

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

NN: EXPRESSED IN LIVER, SIGNAL = 1.4

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

NN: SWISSPROT HIT: P22415, EVALUE 4.00e-14

NN: EXPRESSED IN LIVER, SIGNAL = 1.4

NN: SWISSPROT HIT: AW937895.1, EVALUE 1.00e-14
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tive 0;
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Pred. No. 78;
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SOFTWARE: Annomax Sequence Listi
SEQ ID NO 34172
LENGTH: 65
TYPE: PRT
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Best Local S
Matches 4
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OTHER INFORMATION: EXPRESSED IN
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: ACOMICA-X-1
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  36
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FILING DATE: 2001-01-30
ADDITE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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SYDA
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                                                                                    Conservative
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NUMBER: US 09/632,366
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ED IN ADULT LIVER, SIGNAL = 1.4
ED IN PLACENTA, SIGNAL = 1.2
ED IN HEART, SIGNAL = 1.2
ED IN HEARN, SIGNAL = 1.5
ED IN HEL100, SIGNAL = 1.3
ED IN LUNG, SIGNAL = 1.9
ED IN LUNG, SIGNAL = 1.9
ED IN BONE MARROW, SIGNAL = 1.3
ED IN BT474, SIGNAL = 2.7
AN HIT: AW937895.1, EVALUE 1.00e-16
OT HIT: P22415, EVALUE 3.00e-17
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Pred. No. 78;
0; Mismatches
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US-09-864-761-39908
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US-09-864-761-39908
Query Match
Best Local Similarity
                                                                                                                    FEATURE:
OTHER INFORMATION:
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ESQ ID NO 39908
LENGTH: 65
TYPE: PRT
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR FILING DATE:
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                                                                                OTHER INFORMATION: OTHER INFORMATION:
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/234,687
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5. US20020048763A1
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SEED IN LUNG, SIGNAL = 1.5

SEED IN PLACENTA, SIGNAL = 1.3

SEED IN HEART, SIGNAL = 1.5

SEED IN FETAL LIVER, SIGNAL = 1.4

SEED IN BRAIN, SIGNAL = 1.4
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                                                                              I BONE MARROW, SIGNAL = 1.2
I HELA, SIGNAL = 1.8
I ADULT LIVER, SIGNAL = 1.5
I AM503913.1, EVALUE 1.00e-29
II: p33892, EVALUE 4.00e-08
                       10;
                   Length 65;
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Score Pred.

21; No. DB 78;

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LENGTH: 74
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers.
                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
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APPLICATION NUMBER: PCT/US01/00663
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David K.
                   MAP TO AL035705.14

EXPRESSED IN HEART, SIGNAL = 2.1

EXPRESSED IN BRAIN, SIGNAL = 0.91

EXPRESSED IN LUNG, SIGNAL = 8.7

EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

EXPRESSED IN HELA, SIGNAL = 1.8

EXPRESSED IN HELA, SIGNAL = 1.8

EXPRESSED IN HELA, SIGNAL = 1.8
  EST_HUMAN
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HIT: BE677760.1, EVALUE 1.00e-29
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RESULT 7
US-09-864-761-42544
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Best Local (
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PRIOR FILING DATE: 2001-01
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NOTE: 2000-09-2:
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION: MAP TO AL035705.22'
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELAT, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: Q09137, EVALUE 8.00e-40
OTHER INFORMATION: EST_HUMAN HIT: BE677760.1, EVALUE 1.00e
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PRIOR FILING DATE: 2000-08-03 |
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                                                                                                                FEATURE:
                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                       TYPE:
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APPLICATION NUMBER: US (
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                                                                                                                                                                                                     Engine vers.
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   EVALUE 1.00e-29
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                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47595
LENGTH: 74
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                               LENGTH: 74
TYPE: PRT
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/774,203
OTHER INFORMATION: MAP TO AL035705.16
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.97
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                   ORGANISM: Homo sapiens FEATURE:
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICATION NUMBER: PCT/US01/00661
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Hanzel, David K.
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US-09-864-761-47595
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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                                               TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC025863.2 OTHER INFORMATION: EXPRESSED IN ADULTOTHER INFORMATION: EXPRESSED IN FETAL
                                                                                                 LENGTH:
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                                                                                                                                                                               FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00670
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Chen, Wensheng
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Hanzel, David K.
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IN ADULT LIVER, IN FETAL LIVER,
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Pred. No.
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 SIGNAL
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RESULT 11
US-09-970-088-11
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
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US-09-796-692-1351
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LENGTH: 124
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/218,950 PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
OTHER INFORMATION: EST_HUMAN HIT: BE958511.1, EVALUE 3.00e-40
OTHER INFORMATION: SWISSPROT HIT: Q50028, EVALUE 8.90e-01
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                                                                                                                                                                                              Local Similarity
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Pred. No. 1.5e+02;
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Pred. No. 1.3e+02;
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RESULT 13
US-09-970-088-13
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US-09-970-088-12
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                                                                          Sequence 13, Application US/09970088 Patent No. US20020151489A1 GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 140
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APPLICANT: GRAVEREAUX, EDWIN C.
APPLICANT: SILVER, MARCY
APPLICANT: ISNER, JEFFREY M.
APPLICANT: YOON, YOUNG-SUP
                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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APPLICANT: GRAVEREAUX, EDWIN C. APPLICANT: SILVER, MARCY APPLICANT: ISNER, JEFFREY M. APPLICANT: YOON, YOUNG-SUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-10-02
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APPLICANT: YOON, YOUNG-SUP
TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 71417/55062
CURRENT APPLICATION NUMBER: US/09/970,088
CURRENT FILING DATE: 2001-10-02
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APPLICANT: YOON, YOUNG-SUP
TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 71417/55062
CURRENT APPLICATION NUMBER: US/09/970,088
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,171
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 14
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ilarity 100.0%;
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Pred. No. 1.6e+02;
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US-09-970-088-14
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SEQ ID NO 13
LENGTH: 140
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                Sequence 306, Application US/09881752A Patent No. US20020115078A1
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Best Local :
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                                              APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides
TITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ISNER, JEFFREY M.
APPLICANT: YOON, YOUNG-SUP
TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 71417/55062
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                  APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles
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CURRENT APPLICATION NUMBER: US/09/970,088
CURRENT FILING DATE: 2001-10-02
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CURRENT FILING DATE: 2001-10-02
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 14
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PRIOR FILING DATE: 2000-10-02
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APPLICANT: SILVER, MARCY
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4; Conservative
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Pred. No. 1.6e+02;
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Pred. No. 1.6e+02;
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US-09-881-752A-306
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3939
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 306
LENGTH: 144
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PRIOR TILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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APPLICANT: Rank, David F
APPLICANT: Hanzel, David
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/234,687
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                          PCT/US01/00670
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Pred. No. 1.7
D; Mismatches
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PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 70.59
SOFTMARE: PatentIn ver. 3.0
SEQ ID NO 4419
LENGTH: 175
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4419
     RESULT 18
US-09-738-626-6309
US-09-738-626-6309, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
US-09-864-761-39939
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                                                                                                                                                                                                                                               Query Match
Best Local
APPLICANT: NAKAGAWA, SATOSHI
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: UP 99/377484 PRIOR FILING DATE: 1999-12-16 PRIOR APPLICATION NUMBER: UP 00/159162 PRIOR APPLICATION NUMBER: UP 00/159162 PRIOR FILING DATE: 2000-04-07
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APPLICANT: 'IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
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                                                                                                                                                 119 SYDA 122
                                                                                                                                                                                                                          Local Similarity nes 4; Conserv
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R INFORMATION:
INFORMATION:
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R INFORMATION:
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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                                                                                                                                                                                                                      100.0%; Score 21; DB 9; ilarity 100.0%; Pred. No. 2e+02; Conservative 0; Mismatches
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N: EXPRESSED IN PLACENTA, SIGNAL = 1.9

N: EXPRESSED IN LUNG, SIGNAL = 1.9

N: EXPRESSED IN HEART, SIGNAL = 1.7

N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN BETAL LIVER, SIGNAL = 2.4

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

N: EXPRESSED IN HELA, SIGNAL = 2.7

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

N: SWISSPROT HIT: Q08050, EVALUE 6.00e-83

N: EXTREMENT HIT: AW239326.1, EVALUE 1.00e-76
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                       Length 175;
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ORGANISM: Corynebacterium glutamicum US-09-738-626-5341
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APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKHHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT EILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
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                                                                                                                                                           PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6309
LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5341, Application US/09738626
Publication No. US20020197605A1
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Best Local Similarity
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                          LENGTH: 219
TYPE: PRT
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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YOKOI, HARUHIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEIKO
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100.0%; S
100.0%; P
itive 0;
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Query Match

Best Local Similarity

4;

Conservative

Score 21; DB 9; Pred. No. 2.5e+02;); Mismatches 0;

Length 219; Indels

0;

Gaps

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SYDA 4 |||| SYDA 112

109

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CURRENT APPLICATION NUMBER: US/09/993,308
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/246,349
PRIOR FILING DATE: 2000-11-07
INVMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 256
TYPE: PRT
ORGANISM: Zea mays
US-09-993-308-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT

ORGANISM: Homo sapiens

NAME/KEY: SITE

LOCATION: (7)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-299-958
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US-09-925-299-958
; Sequence 958, Application US/09925299
; Patent No. US20020055627A1
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SEQ ID NO 958
LENGTH: 248
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Matches 4; Conserv
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
                                                                       Matches
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09993308 Patent No. US20020159435A1
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Best Local :
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dilkes, Brian R.
APPLICANT: Sun, Yuejin
TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides
FILE REFERENCE: 1146
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gordon-Kamm, William J.
APPLICANT: Lowe, Keith S.
APPLICANT: Larkins, Brian A.
APPLICANT: Dilkes, Brian R.
138 SYDA 141
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                                  1 SYDA 4
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                                                                     4;
                                                                     Conservative
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                                                                                       100.0%;
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                                                                     0;
                                                                   Score 21; DB 9;
Pred. No. 2.9e+02;
Mismatches 0;
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                                                                                                      Length 256;
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                                                                     Gaps
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; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo s
US-09-808-602-25
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-23
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                    Query Match
Best Local Similarity
Thes 4; Conserve
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US-09-808-602-25
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                                                                                                                                                                           SOFTWARE: PatentIn Ver. SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09808602 Patent No. US20020155115A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                          APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-03-03
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1 SYDA 4
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Shimkets, Richard A
Herrman, John L
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Mezes, Peter S
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Shimkets, Richard A
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Mezes, Peter S
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                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corine A
                                                  100.0%; Score 21; DB 9; 100.0%; Pred. No. 3.1e+02;
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Pred. No. 3.1e+02;
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                                    Mismatches
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                                                                   Length 267;
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                                    Indels
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SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3633
LENGTH: 271
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3633
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 101
LENGTH: 267
TYPE: PRT
                                                                                                               APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PRILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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US-09-738-626-3633
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Best Local Similarity 100.
Watches 4; Conservative
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Patent No. US20020155115A1
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APPLICANT:
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TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richau
APPLICANT: Herrman, John L
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SENOH, AKIHIRO
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Shimkets, Richard A
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Mishra, Vishnu
Mezes, Peter S
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186 SYDA 189

1 SYDA 4

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STRANDEDNESS: Single;

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ
US-09-939-980-462
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US-09-939-980-462
      Matches
                Query Match
Best Local Similarity
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Best Local Similarity 100.
The Conservative
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                                                                                                                                                                            TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 462:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/936,165
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: «Unknown» |
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ward, Judith
Ward, Judith
TITLE OF INVENTION: No. US20020082234Alel Prokaryotic Polynucleotides,
Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                         NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: Fastbeg for Windows Version 2.0
                                                                                                                                                                                                                            TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: King of Prussia
STATE: PA
                                                                                                                                                           LENGTH: 290 amino acids
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   100.0%; ilarity 100.0%; Conservative 0;
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Burnham, Martin
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                                                                                 SEQ ID NO: 462:
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 Score 21; DE Pred. No. 3.3); Mismatches
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 DB 10;
. 3.3e+02;
ches 0;
                                 Length 290;
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 Gaps
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; ORGANISM: Corynebacterium glutamicum US-09-738-626-4308
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                                                                                                                                               FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 7059
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LENGTH: 321
TYPE: PRT
                                                                                            SEQ ID NO 4308
LENGTH: 332
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Best Local Similarity
 Query Match
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APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
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CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
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TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP.
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ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 SYDA 211
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Fernandes, Elma
Shimkets, Richard A
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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Mishra, Vishnu
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 100.0%;
 Score 21;
 DB 9;
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Length 332;
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Query Match
Best Local Similarity
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US-09-815-242-10953
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                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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                                   NUMBER OF SEQ ID NO SOFTWARE: FastSEQ 1 SEQ ID NO 10953 LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10953, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/00
CURRENT FILING DATE: 2001-01-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BATHE, Brigitte TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE maik GENE FILE REFERENCE: 032301 ND 228
                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes
                                                                                                               PRIOR FILING DATE:
                                                                                                                                PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Corynebacterium glutamicum
ORGANISM: Haemophilus influenzae
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314 SYDA 317
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Trawick, John D.
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Zyskind, Judith W.
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                                                                          for Windows Version 4.0
                                                                                                             2001-02-16
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); Mismatches 0;
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Pred. No.
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GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
                                                                                                                                                                                                             RESULT 32
US-09-738-626-4252
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US-09-815-242-10844
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                   Sequence 4252, Application US/09738626 Publication No. US20020197605A1
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Best Local
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Best Local Similarity
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                178 SYDA 181
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Local Similarity 100.0%; Pred. No. 3.
Mismatches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                        1 SYDA 4
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o. US20020061569A1
                              MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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Trawick, John D.
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Zyskind, Judith W.
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; PRIOR APPLICATION NUMBER: 60/186,596; PRIOR FILING DATE: 2000-03-03; NUMBER OF SEQ ID NOS: 114; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 105; LENGTH: 352; TYPE: PRT; ORGANISM: Homo sapiens
             US-09-888-615-95
Sequence 95, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
                                                                                                                                                    B
                                                                                         RESULT 34
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4252
LENGTH: 345
TYPE: PRT
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 105, Application US/09808602
Patent No. US20020155115A1
                                                                                                                                                                                                                                                           Query Match
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APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MacDongall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
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APPLICANT:
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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Mezes, Peter S
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                                                                                                                                                                                                                                       Score 21; DB 9;
Pred. No. 4e+02;
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APPLICANT:

CAENEPEEL, SEAN CHARYDCZAK, GLEN

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; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-95
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US-09-799-777-45
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PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 95
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Best Local Similarity 100.0%;
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APPLICANT: SUDARSANAM, SUCHA
TITLE ONVENTION: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
                                                                             INFORMATION FOR SEQ ID NO: 45:
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                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
                                                                                                                                                  APPLICATION NUMBER: US/09/002,485
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: PF-0459 US
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS NUMBER OF SEQUENCES: 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 PORTER DRIVE
                    LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09799777
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Corley, Neil C.
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baugh, Mariah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sather, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purv
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Pred. No.
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                                                                                                                                                                                                    US-09-815-242-11378
                                                                                                                                                                                                                      RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-738-626-5241
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                                                                                                                                                                     Sequence 11378, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 5241 LENGTH: 360
                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity
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Matches 4; Conserv
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                                                                                                                     APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                             APPLICANT:
                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
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TITLE OF INVENTION:
              TITLE
                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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TATEISHI, NAOKO
SENOH, AKIHIRO
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CLONE: 1988911
                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAYASHI, MIKII
OCHIAI, KEIKO
                                          Carr, Grant J.
Yamamoto, Robert T.
                                                                                         Wall, Daniel
                           Xu, H. Howard
                                                                         Trawick, John D.
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illarity 100.0%;
Conservative C
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              Identification
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Pred. No. 4.1e+02;
); Mismatches 0;
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Pred. No. 4.1e+02;
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              of Essential Genes
                                                                                                                                                                                                                                                                                                                                                            Length 360;
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US-09-738-626-5738
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US-09-815-242-11378
                             Matches
                                                               Query Match
                                                                                                                                                             SEQ ID NO 5738
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Best Local Similarity 100.
Conservative
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                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTMARE: Patentin ver. 3.0
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11378
LENGTH: 360
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                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                               ENGTH:
                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 SYDA 231
1 SYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/257,931
                         4;
                                                                                                                                              378
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TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                        IKEDA, MASATO
                             Conservative
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                           0;
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                                       Score 21; DB 9;
Pred. No. 4.3e+02;
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Pred. No. 4
                           Mismatches
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                                                        Length 378;
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TITLE OF INVENTION: Identification of ES
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITA.011A
CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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Best Local Similarity
Matches 4; Conserv
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 60
LENGTH: 416
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5696, Application US/09815242
Patent No. US20020061569A1
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CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: U.S. NO. U$20020159976A1 09/634,238

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: U.S. NO. U$20020159976A1 09/724,623

PRIOR FILING DATE: 2000-11-28

PRIOR PILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-08-08
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APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Meth
TITLE OF INVENTION: Using Them
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Lactobacillus rhamnosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 SYDA 284
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APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                          Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                         Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                      Xu, H. Howard
                                                                                                                                                                                                                                                                         Yamamoto, Robert T.
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O'Toole, Paul
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Pred. No.
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                                                                                                                                                                                                                                Essential Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5696
LENGTH: 439
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5696
APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT ETIING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078
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US-09-815-242-5045
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US-09-820-893-56
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                                                                                                                                                                                          APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, John D.
APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 56
LENGTH: 491
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/09820893 Patent No. US20020076705A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 21; DB 10; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       Sequence 5045, Application US/09815242 Patent No. US20020061569A1
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/531,119
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/102,895
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: PZ033P1
                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Klebsiella
US-09-815-242-11757
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US-09-815-242-5045
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                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11757
LENGTH: 506
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRStSEQ for Windows Version 4.0
SEQ ID NO 5045
Query Match
Best Local Similarity 100
Matches 4; Conservative
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-10-23
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Zyskind, Judith W.
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      0;
  Score 21; DB 10;
Pred. No. 5.7e+02;
Pred. No. 5.7e+02;
                                        Length 506;
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Sequence 4, Application US/09824735

Patent No. US20020095032A1

GENERAL INFORMATION:
APPLICANT: ZHU, JIAN-KANG
APPLICANT: LIU, JIPING
APPLICANT: ISHITANI, MANABU
APPLICANT: KIM, CHEOL-SOO
TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
FILE REFERENCE: 205645US20
CURRENT APPLICATION NUMBER: US/09/824,735
CURRENT APPLICATION NUMBER: US/09/824,735
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/824,735
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENT APPLICATION NUMBER: US 60/824,735
LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.

ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1909-03-12
NUMBER OF SEQ ID NO 477
SEQ ID NO 477
LENGTH: 549
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US-09-925-302-477
; Sequence 477, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
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                                                                                                                                       ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-824-735-4
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US-09-824-735-4
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Best Local S
Matches 4
                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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LOCATION: (224)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/REY: SITE
LOCATION: (217)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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ORGANISM: Homo sapiens
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225 SYDA 228
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1 SYDA 4
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                                                     ch 100.0%; Score 21; DB 10; 1 Similarity 100.0%; Pred. No. 6.2e+02; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 10; ilarity 100.0%; Pred. No. 6.1e+02; Conservative 0; Mismatches 0;
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                                                                                          DB 10; Length 552;
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Db 282 SYDA 285

Search completed: February 6, 2003, 11:39:44

Job time: 6.83333 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/paa/PCTUS_COMB_pep:*
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                        / cgn2_6/ptodata/1/paa/US083_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US084_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US084_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US086_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US086_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US086_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US089_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US090_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US090_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US092_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US092_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US092_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US093_COMB.pep: *
/ cgn2_6/ptodata/1/paa/US095_COMB.pep: *
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/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
/cgn2_6/ptodata/1/paa/US60_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0	5	4	w	2	1	Result No.
21	21	21	21	21	21	Score
100.0	100.0	100.0	100.0	100.0	100.0	% Query Match Length
9	9	7	7	5	5	% Query Match Length DB ID
-	—	22	7	27	23	BB
PCT-US02-11643-307	PCT-US02-11643-95	2 US-09-867-852-126	US-08-310-912-126	US-60-275-251-178	US-09-908-943A-178	DB ID
Sequence 307, App	Sequence 95, Appl	Sequence 126, App	Sequence 126, App	Sequence 178, App	Sequence 178, App	Description

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5290,	5244,	5109,	4949,	4800,	4799,	4647,	4532,	4448,	4385,	4204,	4149,	4066,	3971,	3910,	3758,	3496,	3306,	3305,	3188,	3161,	3160,	2863,	2862,	2733,	2579,	2398,	2379,	2132,	1988,	1912,	1838,	1760,	1569,	1043,	817,	771,	Sequence 556, App	552,	

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Query Match Best Local Similarity	; OTHER INFORMATION: peptide sequence US-09-908-943A-178	OTHER INFORMATION: Description of Artificial Sequence: synthetic	FEATURE:	ORGANISM: Artificial Sequence	TYPE: PRT	SEQ ID NO 178	SOFTWARE: PatentIn Ver. 2.0	NUMBER OF SEQ ID NOS: 197	PRIOR FILING DATE: 2000-07-19	PRIOR APPLICATION NUMBER: 60/219,795	CURRENT FILING DATE: 2001-07-19	CURRENT APPLICATION NUMBER: US/09/908,943A	FILE REFERENCE: 29915/00281A.US1	EOF	APPLICANT:	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT: Yan, Riqiang	GENERAL INFORMATION:	Sequence 178, Application US/09908943A	US-09-908-943A-178	1
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Score 21; Pred. No.	nce	f Art								795		/908		D AS					•			943A		
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US-08-310-912-126
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CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 126, Application US/08310912 GENERAL INFORMATION:
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY FILE REFERENCE: 29915/00281
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                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,912
FILING DATE:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND
NUMBER OF SEQUENCES: 201
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ausubel, Frederick M. APPLICANT: Staskawicz, Brian J.
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                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2904
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RIOR APPLICATION DATA: APPLICATION NUMBER: 1
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                                CLASSIFICATION:
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Heinrikson, Robert L.
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225 Franklin Street Suite 3100
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Katagiri, Fumiaki
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Pred. No. 4.2e+06;
Mismatches 0;
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                                                                                                         RESULT 5
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Sequence 95, Application PC/TUS0211643
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 126
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APPLICANT: Ausubel, Frederick M.
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Best Local Similarity
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CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR PILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: 08/227,360
PRIOR PILING DATE: EARLIER FILING DATE: 1994-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND TITLE OF INVENTION: DETECTION METHODS FILE REFERENCE: 00786/254002
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 30,162
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Katagiri, Fumiaki
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Pred. No. 4
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Pred. No. 4.2e+06;
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.2e+06;
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 307
LENGTH: 9
TYPE: DRT
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PCT-US02-11643-552; Sequence 552, Application; GENERAL INFORMATION:
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; ORGANISM: Homo Sapiens
PCT-US02-11643-95
                                                            RESULT 7
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR PILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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; TYPE: PRT
; ORGANISM: Homo Sapiens
PCT-US02-11643-552
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PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 556
LENGTH: 9
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 552
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                                                                                                        Query Match
Best Local :
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Best Local Similarity
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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Rubert, Rene S.
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Pred. No. 4.2e+06;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 771
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR PILING DATE: 2001-04-10
PRIOR PILICATION NUMBER: US 60/286,630
PRIOR PILING DATE: 2001-04-25
PRIOR PILING DATE: 2001-04-25
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
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PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
APPLICANT: Morrison, Karen J.
APPLICANT: Morrison, Robert K.
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                                                                                                                                       Gaps
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CT-US02-11643-1569
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; Sequence 1569, Application PC/TUS0211643
; GENERAL INFORMATION:
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PCT-US02-11643-1043
                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version ^{1}4.0 SEQ ID NO 1569
        Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1043

LENGTH: 9
                                                                                                                                                                                                          APPLICANT: JAKOBOVIES, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067-40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR PELICATION NUMBER: US 60,286,630
PRIOR PELICATION NUMBER: US 60,286,630
PRIOR PRIOR PRIOR NUMBER: US 60,286,630
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Matches 4; Conserv
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT #
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
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APPLICANT:
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                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 15017
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PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
                                                                                                        ORGANISM:
                                                                                                                          TYPE: PRT
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                                                                                                                                          LENGTH:
      Local Similarity les 4; Conserv
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Rubert, Rene S.
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Morrison, Robert K.
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      Conservative
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                      100.0%;
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      0;
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                    Score 21; DB 1;
Pred. No. 4.2e+06;
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Pred. | No. 4
    Mismatches
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                                      Length 9;
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    Indels
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Gaps
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                                            PCT-US02-11643-1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1838, Application PC/TUS0211643 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1760
LENGTH: 9
  Query Match
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                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1838
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT /
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT ETLING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT &
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60,286,630 PRIOR FILING DATE: 2001-04-25 NUMBER OF SEQ ID NOS: 15017
                                                                                     LENGTH: 9
TYPE: PRT
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                                                              ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 100.0%; Score 21; DB 1; Local Similarity 100.0%; Pred. No. 4.2e+06; Local Similarity 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SYDA 4
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Rubert, Rene S.
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Rubert, Rene S.
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Morrison, Robert K.
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Morrison, Robert K.
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100.0%; Score 21;
DB
                                                                                                                                                                                                                                                                                                                                               IN TREATMENT AND DETECTION OF CANCER
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Length
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; TYPE: PRT
; ORGANISM: Homo Sapiens
PCT-USO2-11643-1912
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                                                          APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 184P122 USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REPERENCE: $1158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60/286,630

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 15017

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Matches 4; Conserv
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILLING DATE: 2002-04-09
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                       LENGTH: 9
TYPE: PRT
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ORGANISM: Homo Sapiens
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Morrison, Karen J.
Morrison, Robert K.
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Morrison, Robert K.
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APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENUTTIED 184P1E2 USEFUL IN TREATMENT AND

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 15017

SOFTWARE: PastSEQ for Windows Version 4.0
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
NUMBER OF SEQ ID NOS: 15017
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2379
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PCT-US02-11643-2379
PCT-US02-11643-2379
REQUERICE 2379, Application PC/TUS0211643
RESULT 18
RESU
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Best Local Similarity
Thes 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo Sapiens
PCT-US02-11643-2132
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APPLICANT: Raitano, Arth
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S
APPLICANT: Morrison, Kare
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raitano, Arthur B. Faris, Mary Rubert, Rene S. Morrison, Karen J. Morrison, Robert K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ge, Wangmao
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Morrison, Robert K.
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Pred. No. 4.2e+06;
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hes 0;
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
ITILE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
ITILE OF INVENTION: ENTITLED 184P1E2| USEFUL IN TREATMENT AND
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2398
                                                             APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184PLE2 USEFUL IN TREATMENT /
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
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PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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APPLICANT:
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APPLICANT:
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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Morrison, Robert K.
Ge, Wangmao
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Rubert, Rene S.
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Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
Mismatches 0;
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                                                                                                                         TREATMENT AND
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PCT-US02-11643-2862
; Sequence 2862, Application PC/TUS0211643
; GENERAL INFORMATION:
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2579
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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               APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLERIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
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SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SYDA 4
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APPLICATION NUMBER:
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                                                                                                                                      Morrison, Karen J.
Morrison, Robert K.
Ge, Wangmao
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Morrison, Robert K.
                                                                                                                                                                                                                          Faris, Mary
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Pred. No.
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FRSATSEQ for Windows Version 4.0
SEQ ID NO 2863
LENGTH: 9
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PCT-US02-11643-2863
; Sequence 2863, Application PC/TUS0211643
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                                                                                                                                                                                                                                                        PCT-US02-11643-3160
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                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
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                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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APPLICANT:
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APPLICANT:
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APPLICANT: MOTRISON, Karen J.
APPLICANT: MOTRISON, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
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PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
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Local Similarity 100.0%;
hes 4; Conservative 0
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Pred. No. 4.2e+06;
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RESULT 26
PCT-US02-11643-3188
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                                                                                           Sequence 3188, Application PC/TUS0211643
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
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PCT-US02-11643-3161
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                                        APPLICANT:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3161

LENGTH: 9
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       APPLICANT:
                                                                             APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3160
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Best Local :
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TYPE: PRT
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CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR ETLING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR PRIOR PRIOR PLIOR DATE: 2001-04-25
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                     Faris, Mary
Rubert, Rene S.
Morrison, Karen J.
Morrison, Robert K.
Ge, Wangmao
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Jakobovits, Aya
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Morrison, Robert K.
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Pred. No. 4.2e+06;
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APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PRO

TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATM

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-25

INUMBER: OF SEQ ID NOS: 15017

SOFTWARE: FastSEQ for Windows Version 4.0
               PCT-US02-11643-3306

Sequence 3306, Application PC/TUS0211643

GENERAL INFORMATION:
APPLICANT: Chalita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Fone S.
                                                                                                                                                RESULT 28
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PCT-US02-11643-3305
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     APPLICANT:
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Best Local :
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/USO2/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 15017

SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
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Morrison, Karen J.
Morrison, Robert K.
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Karen J.
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                                                                                                                                                                                                                                                              Score 21; DB 1; Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TREATMENT
                                                                                                                                                                                                                                                                                                  Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND DETECTION OF CANCER
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PCT-US02-11643-3758; Sequence 3758, Application PC/TUS0211643; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
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                                                                                                                                                                                                  RESULT 30
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Best Local Similarity 100.0%; Pred. No.
Matches 4; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3496 LENGTH: 9
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR PPLICATION NUMBER: US 60,286,630
PRIOR PPLICATION NUMBER: US 60,286,630
PRIOR PRIOR PRIOR ELING DATE: 2001-04-25
PRIOR PRIOR PRIOR DATE: 2001-04-25
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
        APPLICANT:
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TYPE: PRT
ORGANISM: Homo Sapiens
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Morrison, Robert K.
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Raitano, Arthur B.
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Pred. No. 4.2e+06;
; Mismatches 0;
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Query Match
Best Local Similarity
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LENGTH: 9
TYPE: PRT
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3910
LENGTH: 9
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Best Local Similarity
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APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REPERENCE: 51158-20067.40
CURRENT APPLICATION UMBER: PCC-04-09
CURRENT FILING DATE: 2002-04-09
CURRENT FILING DATE: 2002-04-09
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR SEQ ID NOS: 15017

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT:
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Morrison, Robert K.
Ge, Wangmao
Jakobovits, Aya
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illarity 100.0%;
Conservative (
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                                                                                                    Score 21; DB 1;
Pred. No. 4.2e+06;
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RESULT 32 PCT-US02-11643-3971; Sequence 3971, Ap.

Application PC/TUS0211643

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CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 15017

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4066
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arry
APPLICANT: Rubert, Rene S.
APPLICANT: Morrison, Karen J.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
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APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.
                                                                              Matches
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                            APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR PILING DATE: 2001-04-10

PRIOR PILING DATE: 2001-04-25
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APPLICANT:
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                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                           ORGANISM: Homo Sapiens
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PITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
PITLE OF INVENTION: ENVITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
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                                                                            Conservative
                                                                                            100.0%;
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                                                                                      Score 21; DB 1;
Pred. No. 4.2e+06;
                                                                        Mismatches
                                                                                                           Length 9;
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Best Local Similarity
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PCT-US02-11643-4204
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PCT-US02-11643-4149
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                                                         Matches
                                                                          Query Match
Best Local 9
                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4204
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                                                                                                                                                                                                                                                              APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067-40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Challita-Eid, Pia M. APPLICANT: Raitano, Arthur B.
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APPLICANT:
                                                                                                                                                        TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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TITLE OF INVENTION: ENTITLED 184P182 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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1 SYDA 4
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Faris, Mary
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Morrison, Robert K.
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Morrison, Robert K.
Ge, Wangmao
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Pred. No. 4.2
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Pred. No. 4.2e+06;
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                                                                       4.2e+06;
                                                                                      Length 9;
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Query Match
Best Local Similarity
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PCT-US02-11643-4385
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4385
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184PLE2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CCURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 15017
COMMUNICATION SEQ ID NOS: 15017
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT P
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
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Faris, Mary
Rubert, Rene S.
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Morrison, Robert K.
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Rubert, Rene S.
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                          Conservative
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                100.0%; Score 21; DB 1; I
100.0%; Pred. No. 4.2e+06;
tive 0; Mismatches 0;
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APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 184P122 USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR FILING DATE: 2001-04-10

PRIOR FILING DATE: 2001-04-17

PRIOR FILING DATE: 2001-04-17

PRIOR APPLICATION NUMBER: US 60,286,630

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 15017

SEQ ID NO 4532

LENGTH: 9

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ORGANISM: Homo Sapiens
PCT-US02-11643-4647
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PCT-US02-11643-4532
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                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4647
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Best Local Similarity
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APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT &
FILE REFERENCE: 51158-20067, 40
CURRENT APPLICATION NUMBER: POO2-04-09
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR PRIOR PRIOR PRIOR PRIOR NUMBER: US 60,286,630
PRIOR REPLICATION NUMBER: US 60,286,630
PRIOR REPLICATION NUMBER: US 60,286,630
PRIOR REPLICATION NUMBER: US 60,286,630
PRIOR EPILING DATE: 2001-04-25
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                                                                                                                                    NUMBER OF SEQ ID NOS: 15017
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                                             LENGTH: 9
TYPE: PRT
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Morrison, Robert K.
Ge, Wangmao
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Rubert, Rene S.
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; ORGANISM: Homo Sapiens PCT-US02-11643-4799
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PCT-US02-11643-4799
NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4800
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APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
APPLICANT: Morrison, Karen J.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
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Best Local Similarity
                                                          APPLICANT: JAKODOVIES, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/US02/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US-60/282,739
PRIOR APPLICATION NUMBER: US-60/282,739
PRIOR APPLICATION NUMBER: US-60/286,630
PRIOR APPLICATION NUMBER: US-60,286,630
PRIOR PILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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Best Local
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
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Morrison, Robert K.
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100.0%; Pred. No.
tive 0; Mismatch
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hes 0;
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APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PRO
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREAT!

FILE REFERENCE: 51158-20067.40

CURRENT APPLICATION NUMBER: PCT/US02/11643

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR APPLICATION NUMBER: US 60,286,630

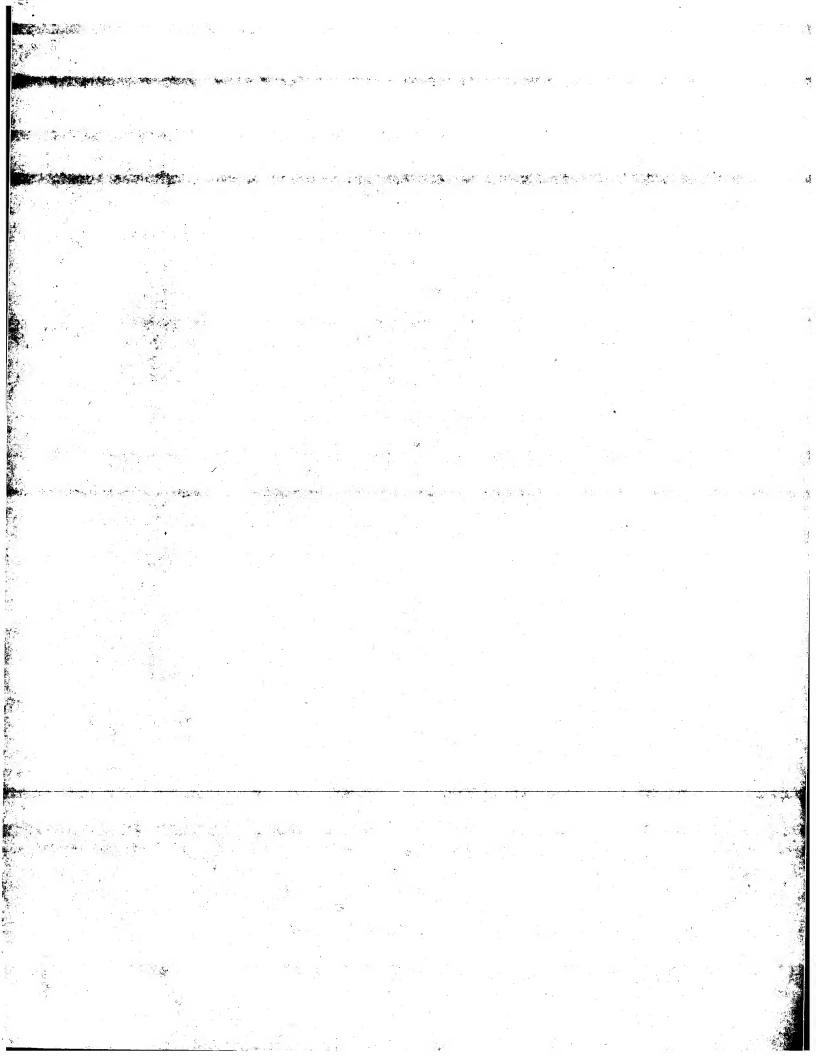
PRIOR FILING DATE: 2001-04-10

PRIOR FILING DATE: 2001-04-25

PRIOR FILING DATE: 2001-04-25
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TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067-40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR PILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEO ID NOS: 15017
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   SEQ ID NOS: FastSEQ for
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Morrison, Robert K.
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Pred. |No. 4.2e+06;
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Pred. No.
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PCT-US02-11643-5244
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SEQ ID NO 5244
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Challita Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 184P1E2 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20067.40
CURRENT APPLICATION NUMBER: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEO ID NOS: 15017
ROPERADER: Exerces for Michael Vocation APPLICATION NUMBER: US 60,286,630
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEO ID NOS: 15017
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENVITLED 184PLE2 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20067.40
CURRENT FALLING DATE: PCT/USO2/11643
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/282/739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
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APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Rubert, Rene S.
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Morrison, Karen J.
Morrison, Robert K.
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Morrison, Karen J.
Morrison, Robert K.
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Search completed: February
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NUMBER OF SEQ ID NOS: 15017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5290
LENGTH: 9
                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                               LENGTH: 9
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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                PCT-US02-41613-292
US-10-203-138A-11128
US-10-203-138A-11208
US-10-203-138A-11208
US-10-276-781-1979
US-09-724-676-67729
US-09-724-676-67724
US-09-724-676-67728
US-09-724-676-67728
US-09-724-676-67728
US-09-724-676-67728
US-09-724-676-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67728
US-09-724-676A-67738
US-09-724-676A-67734
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                                             Sequence 292, App Sequence 1128, A Sequence 1179, Ap Sequence 67729, A Sequence 67724, A Sequence 67726, A Sequence 5736, Ap Sequence 9695, Ap Sequence 95509, A Sequence 25509, A Sequence 25704, A Sequence 25703, A Sequence 67734, A Sequence 6773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII

TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474

FILE REFERENCE: PB 0004 WO 8

CURRENT APPLICATION NUMBER: US/10/203,138A

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR PILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-203-138A-11128; Sequence 11128, Application US/10203138A; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US02-41613-292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 388
SOFTWARE: PatentIn version
SEQ ID NO 292
LENGTH: 64
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Best Local Similarity
Matches 4; Conserv
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100.0%; Score 21; DB 1; ilarity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0;

Length 64;

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RESULT 1 PCT-US02-41613-292 Sequence 292, Ap GENERAL INFORMAT APPLICANT: diab APPLICANT: Mac APPLICANT: Sun APPLICANT: Liu TITLE OF INVENT FILE REFERENCE: CURRENT APPLICAT CURRENT APPLICATI PRIOR APPLICATI PRIOR APPLICATI		44	4 4 4 4 3 2 L	40	3 7	35 36	ω υ 44 υ	ο ω () Ν :	a 30	29	28	27
SULT 1 Sequence 292, Application PC/TUS0241613 Sequence 292, Application PC/TUS0241613 Sequence 292, Application PC/TUS0241613 Sequence 292, Application PC/TUS0241613 APPLICANT: diabexus, Inc. APPLICANT: Sun, Yongming APPLICANT: Liu, Chenghua TITLE OF INVENTION: Compositions and M FILE REFERENCE: DEX-0370 FILE REFERENCE: DEX-0370 CURRENT APPLICATION NUMBER: PCT/US02/4 CURRENT FILING DATE: 2001-12-23 PRIOR APPLICATION NUMBER: 60/343,690 PRIOR FILING DATE: 2001-12-28 NUMBER OF SEC IN NOC: 238			21 100.0	100	100		100	100	21 100.0	100	100.	21 100.0
rtion PC, Inc. Roberto Roberto Inghing			213 5 224 5						184		177	
ethods Relating 1613	ALIGNMENTS		5 US-09-134-000C-3952 5 US-09-134-000C-3952 5 US-09-724-676-97153			US-09-724-676A-67731 US-09-724-676A-67732			1 C	US	US-09-134-000C-	5 US-10-057-498-24114
to Urinary Specific Genes		97153, 97142,	Sequence 3952, Ap Sequence 3952, Ap Sequence 97153, A	16492,	67733, 2328, P			67732,	67730,	6245,	245, A	Sequence 24114. A

(03.08.00)

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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 26 May 2000 (25.05.00)
PRIOR APPLICATION NUMBER: US 09/632.366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR FILING DATE: US 60/234,887
PRIOR APPLICATION NUMBER: US 60/234,887
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                                                                                                                           NUMBER OF SEQ ID NOS: 15438
SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 11208
LENGTH: 65
TYPPE: ^~~
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                                                                                                                                                                                                                                                     PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
FILE REFERENCE: PB 0004 W0 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Molecular Dynamics, Inc.
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LENGTH: 65
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OTHER INFORMATION: EXPRESSED IN BT474,
                                             OTHER INFORMATION: MAP TO AP000044.1
                                                                     FEATURE:
                                                                                        ORGANISM: Homo sapiens
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OTHER INFORMATION:
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FILING DATE: 03 October 2000 (03.10.00)
APPLICATION NUMBER: US 60/236,359
FILING DATE: 27 September 2000 (27.09.00)
APPLICATION NUMBER: US 60/234,687
FILING DATE: 21 September 2000 (21.09.00)
APPLICATION NUMBER: US 09/608,408
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FILING DATE: 03 August 2000 (03.0)
APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel, David
Chen, Wensheng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     David K.
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Pred. No.
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SIGNAL
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ches 0;
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa can be any naturally occurring
US-09-724-676-67729
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US-10-276-781-1979
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; OTHER INFORMATION: SWISSPROT HIT: P22415, EVALUE 3.00e-17
US-10-203-138A-11208
                                                                                                                                                                                                                      FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67729
LENGTH: 73
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILLING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1979
LENGTH: 65
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local
                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)..(12)
LOCATION: Xaa
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, APPLICANT: Tang (
                                                                                                                               OTHER INFORMATION: Xaa can
                                                                                                                                                                                    TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: EST_HUMAN HIT: AW937895.1, EVALUE 1.00e-16
Local Similarity les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 SYDA 40
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          100.0%;
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            Score 21;
Pred. No.
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Pred; No. 1
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              1.7e+02;
                            DB 5;
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1.5e+02;
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Conservative

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Mismatches

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SYDA

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US-09-724-676A-67729

Sequence 67729, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

FILE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181-4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 67729
RESULT 8
US-09-T13-999C-6627
Sequence 6627, Application US/09513999C
; GENERAL INFORMATION:
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US-09-513-999C-6382
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                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-513-999C-6382
                                                                                                                                                                                                                                                            SOFTWARE: Patent.pm
SEQ ID NO 6382
LENGTH: 75
TYPE: PRT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, J.B.
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Pred. No. 1.7e+02;
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1.8e+02;
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                                                              Sequence 67725, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
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Best Local S
Matches 4
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version:
SEQ ID NO 67725
LENGTH: 98
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SEQ ID NO 67724
LENGTH: 98
TYPE: PRT
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SEQ ID NO 6627
LENGTH: 77
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Best Local :
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (11)...(12)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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Pred. No.
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RESULT 11
US-09-724-676-67726
Sequence 67726, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: VARIANTS of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LEGID NO 67726
                                                                                                                                                                                                   RESULT 12
US-09-724-676-67728
; Sequence 67728, Appl:
; GENERAL INFORMATION:
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                                                                APPLICANT: Compage LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67728
LENGTH: 98
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Best Local
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)...(12)
OTHER INFORMATION: Xaa can be
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Best Local
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                                        ORGANISM: Homo sapiens
NAME/KEY: misc_feature LOCATION: (11)..(12)
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OTHER INFORMATION: Xaa
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Pred. No.
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RESULT 14
US-09-724-676A-67725
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OTHER INFORMATION: Xaa can be any naturally occurring amino US-09-724-676A-67724
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOPTWARE: Patentin version 3.2
SEQ ID NO 67724
LENGTH: 98
TYPE: PRT
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing; FILE REFERENCE: 129181.4 Compugen
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                                                                                                                                                                      FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: PatentIn version 3.2 SEQ ID NO 67725
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
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Best Local S
Matches 4
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Best Local Similarity
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   NAME/KEY: misc_feature LOCATION: (14)..(14) OTHER INFORMATION: Xaa
                                                              NAME/KEY: misc_feature LOCATION: (11)..(12) OTHER INFORMATION: Xaa
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OTHER INFORMATION: X
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Pred. No. 2.4e+02;
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RESULT 15
US-09-724-676A-67726
US-09-724-676A-67726
Sequence 67726, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
FILE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67726
LENGTH: 98
TYPE: PRT
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US-09-724-676A-67728
Sequence 67728, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129.81.4 Compugen
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NAME/KEY: misc_feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: Xaa can be any naturally occurring amino US-09-724-676A-67726
                                                                   ; NAME/KEY: misc_feature ; LOCATION: (14) ...(14) ...(14) ...(15) OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-09-724-676A-67728
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67728
LENGTH: 98
TYPE: PRT
   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0
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Best Local
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (11)..(12)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
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Pred. No.
Score 21; DB 5; I
Pred. No. 2.4e+02;
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Pred. No. 2.4e+02;
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PCT-US02-32727-9695
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   RESULT 19
PCT-US02-32727-25509
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LENGTH: 127
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CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
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APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514
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CURRENT FILING DATE: 2002-10-11
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TYPE: PRT
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TYPE: PRT
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Jen, Shyian
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Barth, Brenda
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Bhatia, Ajay
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llarity 100.0%;
Conservative 0
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Pred. No.
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Length 127

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US-09-950-084-7306
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US-10-057-498-25509
Sequence 7306, Application US/09950084

SEQUENCE TIMEORMATION:

APPLICANT: George H. Shimer, Jr.

APPLICANT: George H. Miller

APPLICANT: Roberta S. Hare

APPLICANT: Roberta S. Hare

APPLICANT: Karen J. Shaw

TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods

FILE REFERENCE: 1034/1C963US2
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PCT-US02-32727-25509
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SEQ ID NO 25509
LENGTH: 128
TYPE: PRT
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Best Local :
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LENGTH: 128
TYPE: PRT
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
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APPLICANT:
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CURRENT FILING DATE: 2002-10-11
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APPLICANT: Skeiky,
APPLICANT: Persing,
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514C1
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Ten, Shyian
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Bhatia, Ajay
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Carter, Darrick
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Pred. No. 3.2e+02;
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3.2e+02;
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; ORGANISM: Propionibacterium acnes PCT-US02-32727-29763
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        Matches
                      Query Match
Best Local
                                                                                                                 SEQ ID NO 29763
LENGTH: 157
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SEQ ID NO 7306
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Best Local Similarity
                                                                                                                                                             APPLICANT: Carter, Darrick
APPLICANT: Barth, Brenda
APPLICANT: Barth, Brenda
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION UNDEER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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                                                                                                     TYPE: PRT
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PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1998-03-06
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PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/950,084
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 09/417,811
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TYPE: PRT
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FILING DATE: 1999-03-11
APPLICATION NUMBER: US 09/037,934
FILING DATE: 1998-03-10
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APPLICATION NUMBER: US 09/266,555
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                      Similarity
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Zhang, Siqing
Wang, Siqing
Ten, Shyian
Micha
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Jones, Robert
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Bhatia, Ajay
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Conservative (
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100.0%; P
tive 0;
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                Score 21;
Pred. No.
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Pred. No. 3.2
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    See File Wrapper or PALM

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US-09-724-676A-67734, Application US/09724676A; Sequence 67734, Application US/09724676A; GENERAL INFORMATION: APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing; FILE REFERENCE: 129181.4 Compugen
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67734
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67734
LENGTH: 159
                                                                                                                                                                                              Sequence 24114, Application PC/TUS0232727
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Best Local Similarity
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                                                                                              APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, Dayid
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean
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                                                  APPLICANT:
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                                                              Wang,
                                                                                              Bhatia, Ajay
Maisonneuve, Jean Francois
                                                  Jen, Shyian
                                                                               Zhang, Yanni
Jones, Robert
                  Benson,
                               Lodes, Michael
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Pred. No.
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Pred. No.
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; ORGANISM: Propioni acnes US-10-057-498-24114
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Best Local S
Matches 4
                                                                                                                                                                                                      Sequence GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
AppliCANT: Neiky, Yasir
                                                 NUMBER OF SEQ ID NOS:
SEQ ID NO 24114
LENGTH: 166
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LENGTH: 166
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TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER
EILE REFERENCE: CUB-12 PCT CIP
CURRENT APPLICATION NUMBER: PCT/US02/24310
CURRENT FILING DATE: 2002-710-25
                                                                                                               APPLICANT: Skeiky, Yasir APPLICANT: Persing, David TITLE Office of the Therapy and Diagnosis of FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US01/32354
PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/310,385
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 60/379,866
PRIOR FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 170
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
                                       TYPE: PRT
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Pred. No.
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Query Match

100.0%;

Score 21;

DВ

6

Length 166;

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RESULT 30
US-09-724-676-67730
Sequence 67730, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Enterococcus faecalis US-09-134-000C-6245
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US-09-134-000C-6245
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Sequence 6245, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS
FILE REFERENCE: 032796-032
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                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6245
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6245, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILLING DATE: 1998-08-13
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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TYPE: PRT
ORGANISM: Enterococcus
                                                                                                                                                                             155 SYDA 158
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100.0%; F
tive 0;
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RESULT 32
US-09-724-676-67732
US-09-724-676-67732, Application US/09724676
Sequence 67732, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724;676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
LENGTH: 1184
TYPE: PRT
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RESULT 33
US-09-724-676-67733
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SEQ ID NO 67731
LENGTH: 184
TYPE: PRT
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Best Local S
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Best Local S
Matches 4
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Best Local Similarity
Matches 4; Conserv
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SCETMANDE: DESCRIPTION SERVICES
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67730
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Pred. No. 4.6e+02;
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Pred. No. 4.6e+02;
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Pred! No. 4.6e+02;
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RESULT 34

US-09-724-676A-67730, Application US/09724676A

Sequence 67730, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2

LENGTH: 184
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US-09-724-676A-67731
; Sequence 67731, Application US/09724676A
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                                                                                                                                   ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676A-67731
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67731
LENGTH: 184
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 67733
LENGTH: 184
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                                                         Matches
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                                                                   Local Similarity
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1 SYDA 4
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                                                       100.0%; ilarity 100.0%; Conservative 0;
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                                                   Score 21; DB 5; I
Pred. No. 4.6e+02;
; Mismatches 0;
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Pred. No. 4.6e+02;
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIAN Version 3.2
LENGTH: 184
TYPE: BRT
TYPE: BRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67733, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 67733
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-67733
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US-09-724-676A-67733
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US-09-724-676A-67732
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GENERAL INFORMATION:
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Best Local Similarity
Matches 4; Conserv
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Best Local :
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                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES TITLE OF INVENTION: ENCODED THEREBY FILE REFERENCE: 15966-543 CON
                                                                                                                               CURRENT APPLICATION NUMBER: US/10/218,140
CURRENT FILING DATE: 2002-08-12
                                                                                                                                                                                                                            APPLICANT: Leach, Martin D. APPLICANT: Shimkets, Richa
                                                   PRIOR EPLICATION NUMBER: 60/127,728
PRIOR FILING DATE: 1999-04-05
                                                                                           PRIOR APPLICATION NUMBER: 09/540,763 PRIOR FILING DATE: 2000-03-30
                                   PRIOR APPLICATION NUMBER: 60/127,636
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100.0%; Pred. No. 4.6e+02;
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; ORGANISM: Propioni acnes
US-10-057-498-16492
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US-10-057-498-16492
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; ORGANISM: Propioni acnes
PCT-US02-32727-16492
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PCT-US02-32727-16492
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US-10-218-140-2328
                               CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 16492
LENGTH: 206
TYPE: PRT
                                                                                                                               Sequence 16492, Application US/10057498
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, vasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16492, Application PC/TUS0232727
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean Francois
APPLICANT: Zhang, Yanni
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SEQ ID NO 16492
LENGTH: 206
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NUMBER OF SEQ ID NOS: 6322
SOFTWARE: CUTANATOR VERSION 1.0
SEQ ID NO 2328
LENGTH: 199
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Best Local
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TYPE: PRT
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Ten, Shyian
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Barth, Brenda
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RESULT 43
US-09-724-676-97153
: Sequence 97153, Application US/09724676
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-3952
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US-09-134-000C-3952
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SOFTWARE: PatentIn version
SEQ ID NO 3952
LENGTH: 213
TYPE: PRT
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Best Local (
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SEQ ID NO 3952
LENGTH: 213
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APPLICANT: LYND DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: ENTEROCOCCUS FABCALIS
FILE REFERENCE: 032796-032
CURRENT APPLICATION UMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al | TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
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PRIOR FILING DATE: 1997-08-15
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Pred. No. 5.4e+02;
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TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen

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RESULT 44

US-09-724-676A-97153

Sequence 97153, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: VARIANTS of alternative splicing
FILE REFERENCE: 129181 4. Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 97153

LENGTH: 224

TYPE: PAT

ORGANISM: Homo sapiens

US-09-724-676A-97153
                                                                                                                                             APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2

SEQ ID NO 97142

LENGTH: 231

TYPE: PAT

ORGANISM: Homo sapiens

US-09-724-676-97142
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US-09-724-676-97142
; Sequence 97142, Application US/09724676
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 97153
LENGTH: 224
TYPE: PRT
                                                                     Query Match 100.0%; Score 21; DB 5; I Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 4; Conservative 0; Mismatches 0;
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196 SYDA 199
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Pred. No. 5.7e+02;
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hypothetical prote	probable hsp prote	hypothetical prote	probable sugar-pho	hypothetical prote	protein R09F10.5	ATP synthase b' -	ATP synthase F0, s	single strand DNA	rearranged T-cell	superoxide dismuta	cofilin - yeast (S	probable lipoprote	hypothetical prote	flagellar basal-bo	flagellar basal-bo

Ig H chain V-D-J region (wild-type clone 5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1582

R; Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1582 immunodeficiency in B-less

3

A;Experimental source: bone marrow pre-B lymphocyte C;Keywords: immunoglobulin A; Molecule type: DNA A; Residues: 1-15 <LEV>

Q Query Match
Best Local Similarity
Matches 4; Conserv 1 SYDA 4 100.0%; ilarity 100.0%; Conservative 0; 0 Score 21; DB Pred. No. 25; Mismatches DB 2; Length 15; 0; Indels 0; Gaps

0

밁 φ SYDA 12

hypothetical protein as10716 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AB1896
R;Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
A, Status: preliminary
A, Status: preliminary AB1896 RESULT 2

A; Molecule type: DNA A; Residues: 1-53 <KUR> A; Cross-references: GB GB:BA000019; pIDN:BAB72673.1; pID:g17130061; GSPDB:GN00179 ce: strain PCC 7120

A; Experimental source:

A; Gene: as 10716 Genetics:

Qγ Query Match Best Local S Matches 4 Local Similarity 1 SYDA 4 Conservative 100.0%; 0; Score 21; Pred. No. Mismatches 2; Length 53; Indels 0; Gaps

0

Вb

N

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hypothetical protein Y1075 - Yersinia p
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision
C;Accession: T14992
R;Lindler, L.E.; Plano, G.V.; Burland,
Infect. Immun. 66, 5731-5742, 1998
                                                                                                         RESULT
T14992
                                                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1788
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C:Date: 27-Nov-2001 #sequence_revision
C:Accession: ACI788
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                                                                                                                                                                                                                                                                                                                                    A; Experimental source:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AF065404; NID:g4894216; A;Experimental source: strain Sterne
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A; Residues: 1-67 < OKI>
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Best Local
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Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, Bacteriol. 181, 6509-6515, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones,
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100.0%; Pr
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Pred. No. 1.5e+02;
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No.
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hes 0;
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               G.F.; Blattner,
                                           #text_change
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jurget, O.;
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Fsihi, H.
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C;Date: 10 000. C;Date: 10 000. C;Date: 10 000. C;Date: 10 000. C;Accession: F90808
R;Hayashi, T; Makino, K; Ohnishi, M.; Kurokawa, K.; Ishii, K.; 200
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shii
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Title: Complete genome sequence of enterohemorrhagic Facherichia
                                    A; Molecule type: DNA
A; Residues: 1-84 <HAY>
                                                                                                                                                                                           A; Experimental source:
                      A; Cross-references:
                                                                     A;Status: preliminary
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Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene:
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A; Residues: 1-81 <GLA>
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C; Date: 27-Nov-2001
C; Accession: AD1412
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A;Genome:
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AD1412
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A; Residues: 1-81 <LIN>
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Best Local :
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GB:BA000007; PIDN:BAB34861.1; PID:g13360902; ce: strain O157:H7, substrain RIMD 0509952
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Pred; No.
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                                                                                                                                                                                                                              Escherichia coli (strain 0157:H7,
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1.6e+02;
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surget, O.;
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                 GSPDB:GN00154
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Voss, H.; Wehla
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Score

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Length

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RESULT 10
AB0638
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A;Residues: 1-84 <STO>
A;Cross·references: GB:AE005174; NID:g12514595; PIDN:AAG55806.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
conserved hypothetical protein STY1199 [imported] - Salmonella e C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AB0638
                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A64849
R;Blattner, F.R; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A64849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: B85668
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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;Species: Escherichia coli
;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
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Pred. No. 1.6e+02;
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Pred. No. 1.6e+02;
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hes 0;
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A; Note:
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Query Match
Best Local Similarity
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RESULT 12
T31168
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A;Title: Nucleotide sequence of cDNA for the eclosion hormone A;Reference number: JS0644; MUID:92134263; PMID:1370883
A;Accession: JS0644
A;Molocula Lordon
                                                                                                                                                                      R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic
                                                                                                                                                                                                                             hypothetical protein 392 - Sphingomonas aromaticivorans plasmid C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change C;Accession: T31168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Comment: This neuropeptide controls ecdysis.
C;Cupperfamily: eclosion hormone
F;1-26/Domain: signal sequence #status predicted <SIG>F;27-88/Product: eclosion hormone #status predicted <EV
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s A;Reference number: AB0502; PMID:11677608
                                                                        A; MOIECULE type: DNA
A; Residues: 1-95 < RO
                                                                                                                                                    A; Description: Complete sequence A; Reference number: Z20992
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A; Residues: 1-88 < KAM>
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A; Residues: 1-85 <PAR>
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                                                      A; Cross-references: EMBL: AF079317;
                                                                                                            A; Status: preliminary; translated
                                                                                                                                    A; Accession: T31168
                                                                                                                                                A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:D10135; NID:g217271; PIDN:BAA01012.1;
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                                                        NID:g3378261;
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                                                      PID:g3378309; PIDN:AAD03892.1
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Score Pred.

21; No.

DB 2; 1.9e+02;

Length

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RESULT 15
H84370
hypothetical protein Yng2202h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 680 - Sphingomonas aromaticivorans plasmid pNL1 C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-F C;Accession: T31207 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.T. Sisk F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: sequence extracted from NCBI backbone (NCBIN:113308, NCBIP:113309) C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein F;25-79/Domain: ferredoxin [2Fe-2S] homology <FER>F;40,48,78/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predictions of the covalent of the c
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A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-97 <LEO:
A;Cross-references: GB:M88251; NID:g154545; PIDN:AAA27329.1; PID:g154546
A;Experimental source: PCC 7002
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R; Leonhardt, K.; Straus, N.A.
J. Gen. Microbiol. 138, 1613-1621, 1992
A;Title: An iron stress operon involved in photosynthetic electron A;Reference number: A47673; MUID:92407507; PMID:1527503
A;Accession: C47673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Дb
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tes 4; Conser
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4; Conservative
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2e+02;
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R: Ogata, H.; Audic, S.; Renesto-P. Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution
A: Reference number: A97700; MUID:
A: Accession: D97729
                           A; Molecule type: DNA
A; Residues: 1-115 < KUR>
                                                                                                                                                                                       hypothetical protein RC0236 [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001 C;Accession: D97729
          A; Cross-references:
                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                            D97729
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A; Genome: plasmid
A; Note: plasmid M
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, Cl.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                           RESULT 17
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A; Residues: 1-113 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   salicylate monooxygenase-related protein - Deinococcus radiodurans (strain |
C;Species: Deinococcus radiodurans
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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A;Residues: 1-106 <STO>
A;Cross-references: GB:AE004437;
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Proc. Natl. Acad. Sci. U.S.A. 97, 1218,1218, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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GB:AE006914; PIDN:AAL02774.1; PID:g15619290; GSPDB:GN00173
                                                                                                                                                      Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                    ution in Rickettsia conorii and MUID:21442074; PMID:11557893
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21; DB 2; Pred: No. 2.1e+02;
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thes 0;
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                                                                                                                    Rickettsia prowazekii.
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Maddocks, D.
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.G.; Ja
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A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Reference H95968
A;Recession: H95968
A;Recession: H95968
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                                                              A; Map position:
A; Introns: 25/3
C; Superfamily:
                                                                                                              A; Gene: CESP: K09G1.2
                                                                                                                               A; Experimental source: C; Genetics:
                                                                                                                                                         A;Cross-references: EMBL:Z81101; PIDN:CAB03198.1; GSPDB:GN00023;
                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-127 <WIL>
                                                                                                                                                                                                        A; Status: preliminary; translated from
                                                                                                                                                                                                                       A; Reference number: A; Accession: T23550
                                                                                                                                                                                                                                         submitted to the EMBL Data Library, A; Reference number: Z19758
                                                                                                                                                                                                                                                                            R; Lloyd,
                                                                                                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                                        hypothetical protein K09G1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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A; Residues: 1-121 <KUR>
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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Similarity 100.0%;
4; Conservative 0;
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                                                             Caenorhabditis elegans hypothetical protein K09G1.2
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2.6e+02;
hes 0;
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N.A.; Fisher, R.F.
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RESULT 20
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C; Superi
C;Accession: Ĉ89791
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; S
                                                       C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S77545
R;Kaneko, T.; Sato, S.; Kotani, O, K.; Okumura, S.; Shimpo, S.; DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90733
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hayashi, T.; Makino, K.; Ohnishi, M.;
gasawara, N.; Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable minor tail protein [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                       hypothetical protein [imported] - Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                   A; Note:
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A; Residues: 1-129 <KAN>
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A; Residues: 1-128 <HAY>
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Best Local
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    Synechocystis sp.

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Shiba, T.; Hattori,
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Shinagawa,
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       Sekimizu,
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A;Gene: CAC1919
C;Superfamily: bacterial single-stranded DNA-binding protein; single-stranded DNA-bindin
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                                                                         A;Cross-references: GB:AE001437; PIDN:AAK79882.1; A;Experimental source: Clostridium acetobutylicum
                                                                                                                   A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KUR>
                                                                                                                                                                      A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A98900; MUID:21359325; PMID:21359325
A;Accession: G97136
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iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85583
A;Status: preliminary
A;Molecule type: DNA
A:Basidings 11-129 / CMPON
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C;Superfamily: phage lambda minor tail protein G
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                                                               Genetics:
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A; Residues: 1-130 < KUR>
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et 357, 1225-1240, 2001
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. 2.7e+02;
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ATCC824
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                                                                                                                                                                                                                                                                           K.S.; Zeng, Q.; Gibson,
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uncharacterized conserved protein CAC2767 [imported] - Clostridium acetobutylicum C;Speciaes: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: D97240
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
                                                                                                     RESULT
D97240
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                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:282076; NID:e1247330; PIDN:CAB04936.1; GSPDB:GN00020; CESP:W
                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-133 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T26268
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted to the EMBL Data A; Reference number: Z20186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein W07G1.4 - Ca
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_rev
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T26268
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T35218
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A; Residues: 1-133 <S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; submitted to the EMBL Data Library, September 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T35218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
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Pred. No. 2.7
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Pred. No. 2.7e+02;
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Pred: No. 2.7e+02;
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Markarova,
Smith, D.R.
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Koonin,

E. V. ;

Smith,

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J. Bacteriol. 183, 4023-4030, 2007
A;Title: Genome Sequence and Comparative Analysis of the Solvence Indianaly A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97240
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-133 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80711.1; PID:g15025804; GSPDB:GN00168
A;Cross-references: GB:AE001437; PIDN:AAK80711.1; PID:g15025804; GSPDB:GN00168
A;Cross-references: GB:AE001437; PIDN:AAK80711.1; PID:g15025804; GSPDB:GN00168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rearranged T-cell receptor delta-chain/ Vdelta5.2-Ddeltas-Jdelta1 - C:Species: Sus scrofa domestica (domestic pig) C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-C:Date: 21-Feb-1997 #sequence_revision 21-Feb-
                                                                                                                                                                                                                                                                                                               C;Accession: I46643
R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in A;Reference number: I46623; MUID:95363165; PMID:7636249
A;Accession: I4664
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-134 <STO>
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Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: B87162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable secreted protein [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Decies: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_chcC;Accession: B87162
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A; Residues: 1-135 < YAN>
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                                                                                                                                    F;32-112/Domain:
                                                                                                                                                              ;Superfamily: immunoglobulin V region; Keywords: T-cell receptor
                                                                                                                                                                                            Cross-references: GB:D49584; NID:g1041170; PIDN:BAA08528.1; PID:g1041171; Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No.
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Pred. No.
Score 21; DB 2;
Pred. No. 2.8e+02;
Mismatches 0;
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2.7e+02;
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A; Map position:
C; Superfamily: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                             flagellar basal-body rod protein [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
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C; Superfamily: I
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c;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: E97426
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E97426
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A; Residues: 1-139 < KUR>
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A;Molecule type: DNA
A;Residues: 1-139 <KUR>
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A;Accession: E97426
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Science 294, 2323-2328, 2001
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                                                                                                                                                                A;Gene: flgC
                                                                                                                                                                                                                                                                                                                                                A; Authors: Yoo, H.; Tao, Y.; Biddle,
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Doughty, D.
                                                                                 No.
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protein HI0589 -

Haemophilus influenzae (strain

Rd KW20)

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C; Accession: F70661

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Ratture 393, 537-544, 1998

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A; Accession: F70661

A; Accession: F70661

A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                              cofilin - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L0595; protein YLL050c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
C;Accession: A44397; B44397; JN0529; S64802; S50970; S31309; S36087
                                                             R;Moon, A.L.; Janmey, P.A.; Louie, K.A.; Drubin, D.G. J. Cell Biol. 120, 421-435, 1993
A;Title: Cofilin is an essential component of the yeast A;Reference number: A44397; MUID:93132073; PMID:8421056
A;Reference number: A44397;
A;Accession: A44397
A;Molecule type: DNA
A;Residues: 1-143 <MOO>
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A; Residues: 1-139 <COL>
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Accession: B64010
A; Stratus.
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A; Residues: 1-139 <TIGR>
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Escherichia coli sigma-E factor regulatory protein
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nilarity 100.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0%;
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Pred. No.
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ches 0;
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                                                                                   cortical cytoskeleton
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C;Accession: T44910
R;Dennis, P.P.; Shimmin, L.C.
R;Dennis, P.P.; Shimmin, L.C.
R;Dennis, P.P.; Shimmin, L.C.
R;Cennis, P.P.; 
                                                                                                            A; Gene: sod1
C; Superfamily:
C; Keywords: met.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns:
C; Superfami
                                                                                                                                                                                                                                                                                               A; Molecule type: I
A; Residues: 1-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              superoxide dismutase (EC 1.15.1.1) (Fe) [similarity] - Haloferax mediterranei (fragme
C;Species: Haloferax mediterranei
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 24-Oct-2000
                                                                                                                                                                                                                                                              A; Cross-references:
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F; 88-118/Region:
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A;Cross-references: SGD:S0003973; MIPS:YLL050c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 'MWGKKFIRSQENVKFLCS', 6-143 <WEW>
A;Cross-references: EMBL:Z47973; NID:g642313; PIDN:CAA88007.1;
C;Comment: Cofilin reversibly regulates actin polymerization ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:D13230; NID:g287599; PIDN:BAA02514.1; PID:g287600 R;Wedler, H.; Wedler, S.; Scharfe, M.; Wambutt, R. submitted to the Protein Sequence Database, May 1996 A;Reference number: S64792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 43-56;83-96,'X',98;106-129,'DS',132-141 <MO2>A;Note: sequence extracted from NCBI backbone R;Iida, K.; Moriyama, K.; Matsumoto, S.; Kawasaki, H.; Ni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 12L
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A;Title: Isolation of a yeast essential gene, COF1, that encodes a homologue of mamma A;Reference number: JN0529; MUID:93178959; PMID:8440472
A;Accession: JN0529
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A;Note: experimental_source strain S288C
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A; Residues: 1-143 <WED>
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A; Residues: 1-143 <IID>
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   Query Match
Best Local Similarity
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Best Local
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talloprotein;
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                                                                                                                                                                                                                                                                                                   <DEN>
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100.0%;
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n; oxidoreductase
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   Score 21;
Pred. No.
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3e+02;
                                     DB 2;
                                                                                                                                                                                                                                                  PIDN: AAB60932.1; PID: g2190598
                             Length 144;
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Conservative

0;

Mismatches

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Gaps

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single strand DNA binding protein, SSB [imported] - Clostridium acetobutylicum C;Specles: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: H97356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in A;Reference number: 146623; MUID:95363165; PMID:7636249
A;Accession: 146642
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rearranged T-cell receptor delta-chain/Vdelta5.1-Ddeltas-Jdelta1 - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999 C;Accession: I46642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, F.; Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the A; Reference number: A96900; MUID:21359325; PMID:21359325
C;Accession: A64662
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mcison, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997
                                                                                             ATP synthase F0, subunit b' - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-144 <KUR>
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A; Residues: 1-144 < YAN>
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A64662
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100.0%; F
itive 0;
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3e+02;
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ATCC824
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                                                                                                 08-Oct-1999
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              A.; McKen
Watthey,
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                                   McKenne
                                                          R.D
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                                     Query Match
Best Local
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ьосаl

Similarity 4; Conserv

100.0%; llarity 100.0%; Conservative 0

0

Mismatches

0

Indels

0,:

Gaps

0;

Score 21; Pred. No.

3e+02;

DB 2;

Length 145;

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C; Accession: A71856

R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G. Nature 397, 176-180, 1999

Nature 397, 176-180, 1999

A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric A; Reference number: A71800; MUID:99120557; PMID:9923682

A; Accession: A71856
                                                                                                                                                                                                                                                                                                                          protein R09F10.5 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
A71856
                                                                                                                                                 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: H89587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64662
A; Map position:
                                                                                      A; Molecule type: DNA
A; Residues: 1-145 <S
                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                 R; anonymous, The C. elegans (
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                   H89587
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A; Residues: 1-144 <A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP synthase b' - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE000619; GB:AE000511; NID:g2314276; PIDN:AAD08179.1; PID:g231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-144 < TOM>
                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Experimental source:
                                             Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
                         Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; ilarity 100.0%; Conservative
                                                                                    <STO>
                                                                                                                                                                                                                                                                                   elegans Sequencing
                                                               GB:chr_x;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain J99
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                                                               PIDN:AAC69094.1; PID:g1465853; GSPDB:GN00028;
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Pred. No. 3e+
); Mismatches
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                                                                    CESP: R09F
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A;Cross-references: GB:AL591985; PIDN:CAC48757.1; PID:g15140230; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, M. Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; pMID:11474104
밁
                                   δÃ
                                                                                                                                                                                                                          A; Gene: SMb20371
                                                                                                                                                                                                                                                                     A; Contents: annotation
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A; Residues: 1-148 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C:Accession: E95886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable sugar-phosphate isomerase protein [imported] - Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
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E95886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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A;Accession: F81272
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A; Residues: 1-145 < PAR>
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                                                                                                                                 Query Match
                                                                                                                                                                         Superfamily: galactoside O-acetyltransferase
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Best Local Similarity
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34
                                                                                    Local Similarity
nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                          1 SYDA 4
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SYDA 37
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                                                                                    Conservative
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Pred. No.
                                                                                    Mismatches
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                                                                                                  DB 2;
3e+02;
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                                                                                                                          Length 148;
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                                                                               Indels
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1, S.; Barrel
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A;Status: preliminary

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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.
A;Title: Deciphering the biology of Mycobacterium tuberculosis A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: G70939

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: hsp
C;Superfamily: alpha-crystallin
A; Accession: G97723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable hsp protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AL021929; GB:AL123456;
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-159 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown;
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A; Introns: 70/1; 100/3; 132/3
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C;Date: 15-Oct-1999 #sequence_revision
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A; Residues: 1-158 <WIL>
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A; Molecule type: DNA
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C; Genetics:
A; Gene: RC0191
C; Superfamily: 4-hydroxyphenylacetate 3-monooxygenase small chain
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
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                                                                                                                                                                                                                                                                                           ECLOSION HORMONE.
BY SIMILARITY.
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A -> S (IN REF. 2).
S -> G (IN REF. 2).
Q -> E (IN REF. 2).
AR -> FK (IN REF. 2).
KD -> DL (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                  Score 21;
Pred. No.
                                                                                                                                                                                                                                                                          429DDC0ADDAAD852 CRC64;
                PRT;
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ion update)
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                                                                                                                                                                                                                    68;
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There are no restrictions
ng as its content is in
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of the silkworm,
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Lepidoptera; Glossata;
                                                                                                                                                                                               0;
                                                                                                                                                                                                                                  Length 88;
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SO TETERAR REPRESENTATION OF THE PROPERTY OF T
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                       PER_LOXAL
Q25221;
                                      Chalmers D.
                                                                                                                                                                                       Eukaryota; Metazoa;
Insecta; Pterygota;
                                                                                                                                                                                                                                                                PER.
                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence | 15-JUL-1999 (Rel. 38, Last annotatio Period circadian protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
METAL
METAL
                                                                                SEQUENCE FROM N.A. MEDLINE=95115533;
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01-JUL-1993
01-JUL-1993
                                                             Nielsen J.,
                                                                                                                                                                       Muscomorpha; Diopsoidea;
           Big flies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M88251; AAA27329.1; -. PIR; C47673; C47673. HSSP; P27320; IDOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions are nowed. Usage by and modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                    oxocera albisata (Rust fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
-!- COFACTOR: BINDS 1 2FE-2S CLUSTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the marine cyanobacterium Synechococcus sp. J. Gen. Microbiol. 138:1613-1621(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synechococcus sp. (strain
Bacteria; Cyanobacteria; C
NCBI_TaxID=32049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00111; fer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000564; 2Fe2S_ferredoxin.
InterPro; IPR001041; Ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leonhardt K.G., Straus N.A.;
"An iron stress operon involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92407507;
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39 39 IRON-SULFUR (2:
44 44 44 IRON-SULFUR (2:
47 47 IRON-SULFUR (2:
77 77 IRON-SULFUR (2:
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             small repeats: the
                                                         Peixoto
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                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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38, Last sequence update)
38, Last annotation updat
                                                                                PubMed=7815924;
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26,
                                                                                                                                                         Arthropoda; Mandibulata;
Neoptera; Endopterygota;
idea; Psilidae; Psilinae;
                                                         A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10258 MW;
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, Last sequence up
, Last annotation
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IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
71F366CA9DF42549 CRC64;
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                                                      A., Costa R., Kyriacou C.P.,
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                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
             region
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                                                                                                                                                                Pancrustacea; Hexapoda; Diptera; Brachycera; Loxocera.
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           of the
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                                                     MEDLINE=97305158; PubMed=9161424; Deakin W.J., Furniss C.S., parker V.E., Shaw "Isolation and characterisation of a linked Agrobacterium tumefaciens encoding proteins basal-body structure."; Gene 189:135-137(1997).
                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-97305158; Pubme
Deakin W.J., Furniss C
                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Flagellar basal-body rod protein flgC.
FLGC OR ATU0554 OR AGR_C_975.
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                                                                                                                                                                                                                                                                                                                                                                               Q44336;
                                                                                                                                                                                                                                                                                                                                                                                                 FLGC_AGRT5
SEQUENCE FROM N.A. MEDLINE-21608550;
                                                                                                                                                                                                       Rhizobiaceae; Rhiz
NCBI_TaxID=176299;
                                                                                                                                                                                                                                           Agrobacterium tumefaciens
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biological rhythms; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U11806; AAA76593.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIRECT TRANSCRIPTIONAL INHIBITION (BY SIMILARITY).

SUBBURIT: FORMS HETERODIMER WITH TIMELESS (TM); THE COMPLEX THEN TRANSLOCATES INTO THE NUCLEUS (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR AT SPECIFIC PERIODS OF THE DAY.

FIRST ACCUMULATES IN THE PERINUCLEAR REGION ABOUT ONE HOUR BEFORE TRANSLOCATION INTO THE NUCLEUS. INTERACTION WITH TIM IS REQUIRED FOR NUCLEAR LOCALIZATION (BY SIMILARITY).

FOR NUCLEAR LOCALIZATION (BY SIMILARITY).

PTM: PHOSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLICATED IN THE STABILLTY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHYTHMICITY OF LOCOMOTOR ACTIVITY, ECLOSION BEHAVIOR, AND FOR THE RHYTHMIC COMPONENT OF THE MALE COURTSHIP SONG THAT ORIGINATES IN THE THORACIC NERVOUS SYSTEM. THE BIOLOGICAL CYCLE DEPENDS ON THE RHYTHMIC FORMATION AND NUCLEAR LOCALIZATION OF THE TIM-PER COMPLEX. LIGHT INDUCES THE DEGRADATION OF TIM, WHICH PROMOTES ELIMINATION OF PER. NUCLEAR ACTIVITY OF THE HETERODIMER COORDINATIVELY REGULATES PER AND TIM TRANSCRIPTION THROUGH A NEGATIVE FEEDBACK LOOP. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: ESSENTIAL FOR BIOLÓGICAL CLOCK FUNCTIONS: DETERMINES THE PERIOD LENGTH OF CIRCADIAN AND ULTRADIAN RHYTHMS; AN INCREASE IN PER DOSAGE LEADS TO SHORTENED CIRCADIAN RHYTHMS AND A DECREASE LEADS TO SHORTENED CIRCADIAN RHYTHMS. ESSENTIAL FOR THE CIRCADIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||
| SYDA 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109
109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evol. 11:839-853(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                         Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
 PubMed-11743193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11600 MW;
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                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                           (strain C58 / ATCC 33970).
alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21;
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                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                Shaw C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                            involved
                                                                                                                cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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1 flagellar
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SOS DE PER DE ROS

01-NOV-1995 (01-NOV-1995 (15-JUN-2002 (Hypothetical HI0589

(Rel. 32, Created)
(Rel. 32, Last sequence up
(Rel. 41, Last annotation
1 protein HI0589.

update)

update)

Haemophilus influenzae.
Bacteria; Proteobacteria;

gamma

subdivision;

Pasteurellaceae;

Y589

Y589_ HAEIN

HAEIN

STANDARD;

PRT;

139

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P44020;

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Matches
                                                                                                                                                         Query Match
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Cielo C. Slater S.;

Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";

Science 294:2323-2328(2001).

-i- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L.p. S. AND M) MOUNTED ON A CENTRAL ROD. THE ROD CONSISTS OF ABOUT 26 SUBUNITS (FLGG IN THE DISTAL PORTION, AND FLGG FLGG AND FLGF ARE THOUGHT FLGG IN THE DISTAL PORTION OF THE ROD WITH ABOUT 6 SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                               CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                    EMBL; U39941; AAB68966.1; -. EMBL; U95165; AAB71788.1; -. EMBL; AE009024; AAL41571.1; -. EMBL; AE007990; AAK86366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=21608551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nester E.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood D.W., Setubal J.C., Kaul
                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                Flagella; Complete proteome.
                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                 InterPro; IPR001444; Flag_bb_rod.
PROSITE; PS00588; FLAGELLA_BB_ROD;
                                                  113 SYDA 116
σ
                                                                                                                                        Local
                                                                                    1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE FLAGELLA BASAL BODY ROD PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUILD UP THE PROXIMAL PORTION OF THE EACH (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294:2317-2323(2001).
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4; Conser
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101
139 AA;
                                                                                                                      100.0%; llarity 100.0%; Conservative 0;
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15100
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L -> V (IN REF. 1).
                                                                                                                        Score 21; DE
Pred. No. 1.1
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                                                                                                                                       1.1e+02;
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                                                                                                                                                           Length 139;
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COFI_YEAST
ID COFI_YEAST
AC Q03048;
DT 01-JUL-1993
DT 01-JUL-1993
DT 15-JUN-2002
DE Cofilin.
GN COFI OR YLL
OS Saccharomyce
OC Eukaryota;
OC Saccharomyce
OC Saccharomyce
OX NCBI_TaxID=-
RN MEDLINE=931;
RA MOON A.L.;
RT "ISOLATION GRA
RA MEDLINE=931;
RA MEDLINE=931;
RA MEDLINE=931;
RA SEQUENCE FRC
RM [2]
RP SEQUENCE FRC
RM [2]
RA Yahara I.;
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Best Local S
Matches 4
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01-JUL-1993
01-JUL-1993
15-JUN-2002
                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE=93132073; PubMed=8421056; Moon A.L., Janmey P.A., Louie K.A., "Cofilin is an essential component c
                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacclaromycetales; Saccharomycetaceae; Saccharomyces
                                                                         SEQUENCE FROM N.A. MEDLINE=93178959;
                                                                                                                                                                  cytoskeleton."
                                                                                                                                                                                                                                                                                                                                                                                                COFILIN.
COF1 OR YLL050C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32740; AAC22246.1; TIGR; HI0589; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restitute
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95350630; PubMed=7542800;
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                                                                                                                                               Cell Biol.
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97
139
         of a
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(Rel. 26, Last sequence update)
(Rel. 41, Last annotation updat
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         yeast
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                                                                         PubMed=8440472;
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117
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  essential gene,
                                                   Matsumoto
                                                                                                                                                                                     component of
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6C26821FAF4DF32D
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                                                 s:
                                            Kawasaki H., Nishida
                                                                                                                                                                                                                                                          43-56;
                                                                                                                                                                                                             Drubin D.G.;
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  COF1,
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ches 0;
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that encodes a homologue
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                                                                             Query Match
Best Local :
                                                              Matches
                                                                                                                            Actin-binding; Cytoskeleton; 3D-structure.

DOMAIN 90 109 ACTIN-BINDING
SEQUENCE 143 AA; 15901 MW; 7A03747B0F2
                                                                                                                                                                                                       InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofilin_ADF; 1.
ProDom; PD002129; Actbind_cofin; 1.|
                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib!ch).
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                                                                                                                                                                         SMART; SM00102; ADF; 1. PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Struct Biol. 4:366-369(1997).

"I FUNCTION: CONTROLS REVERSIBLY ACTIN POLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x-ray Crystallography (2.3 angstroms).
medline=97290449; pubmed=9145106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodal A.A., Tetreault J.W., Lappalainen P., I "Aiplp interacts with cofilin to disassemble J. Cell Biol. 145:1251-1264(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein.";
Gene 124:115-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of mammalian cofilin, a low-M(r) actin-binding and depolymerizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10366597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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49
                                                                                                                                                                                                                                                      BL; Z14971; CAA78694.1; -.
BL; Z13230; BAA02514.1; -.
BL; Z73155; CAA97502.1; -.
BL; Z73155; A44397
R; A44397; A44397
R; S31309; S31309.
R; JN0529; JN0529.
B; 1COF; 01-APR-97.
B; 1COF; 08-JUN-99.
B; 1COP; 08-JUN-99.
B; 1COP; 08-JUN-99.
                            1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Interacts with actin and AIP1 in a ternary complex. SUBCELULAR LOCATION: THROUGHOUT THE CYTOPLASM (BUT NOT ON T CYTOPLASMIC CABLES) AND MAJOR COMPONENT OF THE CORTICAL ACTIC CYTOSKELETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: THE N-TERMINUS SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: THE N-TERMINUS IS BLOCKED. | SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEIN SIMILAR TO THE N-TERMINUS OF YEAST ABPI PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND
DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO
BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
MAJOR COMPONENT OF INTRANUCLEAR! AND CYTOPLASMIC ACTIN RODS. IN
EFFECT, YEAST COFILIN INCREASES, THE RATE OF ACTIN POLYMERIZATION
BY MAKING NEW ENDS AVAILABLE FOR ACTIN SUBUNIT ADDITION. SUCH A
PROTEIN COMPLEX IS IMPORTANT FOR THE POLARIZED GROWTH OF YEAST
SYDA 52
                                                              4;
                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAY-1996)
                                                              Conservative
                                                                           100.0%;
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To the EMBL/GenBank/DDBJ
                                                            0;
                                                                                                                          ACTIN-BINDING (POTENTIAL); 7A03747B0F21F22D CRC64;
                                                                           Score 121;
Pred. No.
                                                         Mismatches
                                                          . 1.2e+02;
ches 0;
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e actin filaments.";
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                                                                                        Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF FAMILY.
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RESULT 8
SOD1_HALME

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ALD DESCRIPTION OF THE PROPERTY OF THE PROPERT
RESULT 9
GALX_CANMA
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Best Local
                                                                                                                                                                                            GALX_CANMA STAN
P56600;
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
15-JUN-2002 (Rel. 4
    Eukaryota; Fung1; Ascomycota;
Saccharomycetales; mitosporic
NCBI_TaxID=5479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            008461;
008461;
30-MAY-2000 (Rel. 39, Createq)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
GALIO bifunctional protein [includes: UDP-glucose 4-
(EC 5.1.3.2) (Galactowaldenase); Aldose 1-epimerase
(Mutarotase)] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics titute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001189; SODismutase
Pfam; PF00081; sodfe; 1
Pfam; PF02777; sodfe_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U78908; AAB60932.1; HSSP; P80857; ISSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           archaea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97257269; PubMed=9106366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Halo Halobacteriaceae; Haloferax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOD1_HALME
008461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Evolutionary divergence and salinity-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dennis P.P., Shimmin L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      71 SYDA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD000475; SODismutase; PS00088; SOD_MN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
42
124
128
144
144
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                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manganese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15613 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MANGANESE LIGAND
MANGANESE LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21;
Pred. No.
                                         Saccharomycotina; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47BBA0AC551A09A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                         153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
(BY SIMILARITY).
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                                         Saccharomycetes; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                    4-epimerase
se (EC 5.1.3.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RIB2_PHOLE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                  RIB2_HOLE STANDARU;
Q93E52;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.
(Lumazine synthase) (Riboflavin synthase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        Lin J.-W., Chao Y.-F., Weng S.-F.; Riboflavin synthesis genes ribE, ribB, ribH, ribA reside operon of Photobacterium leiognathi."; Biochem. Biophys. Res. Commun. 284:587-595(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01370; Epimerase; 1.
Pfam; PF01370; Epimerase; 1.
PROSITE; PS00545; ALDOSE_1_EPIMERASE; PARTIAL.
PROSITE; PS00545; ALDOSE_1_EPIMERASE; NAD; Galactose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D29759; -; NOT_ANNOTATED_CDS.
HSSP; P09147; IXEL.
InterPro; IPR001823; Ald1_epimerase.
InterPro; IPR001823; Epimerase_Dh.
InterPro; IPR000205; NAD_binding.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Park S.M., Ohkuma M., Masuda Y., Ohta A., Takagi M. "Galactose-inducible expression systems in Candida promoters of newly-isolated GAL1 and GAL10 genes.";
                                                              STRAIN=PL741;
MEDLINE=21290647;
                                                                                                                Photobacterium.
NCBI_TaxID=658;
                                                                                                                                                         Photobacterium leiognathi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>'</del>
                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reast 13:21-29(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97197967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 40 SYDA 43
                                                                                                                                                                                                                                                                                                                                                          1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Galactose metabolism; third step.
PATHWAY: Hexose metabolism.
SIMILARITY: THE N-TERMINAL SECTION; BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPIMERASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ALDOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Mutarotase converts alpha-aldose to the is active on D-glucose, L-arabinose, D-xylose, D-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPIMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        153
153 AA;
                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme;
>153
                                                              PubMed=11396941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9046083;
                                                                                                                                                                                                                                                                                                                                                                                                                                        16752 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isomerase; NAD; Galaci
GALACTOWALDENASE
                                                                                                                                          gamma
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        A069AC3040BC978D
                                                                                                                                             subdivision;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-D-glucose
                                                                                                                                            Vibrionaceae;
                                                                                                                                                                                  chain).
                                                                                                                                                                                                                                                                                                                                                                                                             Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maltosa
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                                                                                                                                                                                               (DMRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-anomer.
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                                     'n
                                                                                                                                                                                                synthase
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                                                                                                                                                                                                                                                                                                                                                                                    0
                                     the
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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FUNCTION: Riboflavin synthase is a bifunctional enzyme

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RESULT 11
RL2B_TRYBB
ID 201-FI
DT 01-FI
CO REL2:
GN REL2:
GN REL2:
GN REL3:
GN REBDI
RN (1]
RN (1]
RN (1]
RN (1]
RN (1)
RN MEDI

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Best Local
                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as the content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RL2B_TRYBB
P41165;
O1-FEB-1995
O1-FEB-1995
O1-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94232821; pubMed-8177742;
Metzenberg S., Joblet C., Verspieren P., Agabian
"Ribosomal protein L25 from Trypanosoma brucei: p
molecular co-evolution of an rRNA-binding protein
binding site.";
Nucleic Acids Res. 21:4936-4940(1993).
-1- FUNCTION: THIS PROTEIN BINDS TO A SPECIFIC RE
                           EMBL; L21172; AAC37186.1; -.
InterPro; IPR001014; Ribosomal_L23.
Pfam; PF00276; Ribosomal_L23; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ISTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _TRYBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma brucei brucei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPL23A OR RPL25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60S ribosomaı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00885; DMRL_synthase; ProDom; PD003664; DMRL_synthas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGRO0114; ribH; 1.
Riboflavin biosynthesis; Transferase
SEQUENCE 156 AA; 16423 MW; B53E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002180; DMRL_synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF364106; AAK83294.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 SYDA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SYDA 4
                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity). CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-lumazine (By similarity) riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS PROTEIN BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a case the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 (Rel. 31, 0
5 (Rel. 31, 1
6 (Rel. 33, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                  Ribosomal_L23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein L23A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               21:4936-4940(1993)
PROTEIN BINDS TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB 1;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B53E2727C6BCD0A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions one as its content is in
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rRNA
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HXD3_BRARE
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                                                    Query Match
Best Local
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Matches
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                                                                                           DNA_BIND
NON_TER
SEQUENCE
                                                                                                                                                                                                            PRINTS; PRO0024; HOMEOBOX.
PRINTS; PR00021; HTHREPRESSR.
PRINTS; PR00031; HTHREPRESSR.
PR0000010: Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                  Transcription NON_TER
                                                                                                                                                                        PROSITE; PS00027; PROSITE; PS50071;
                                                                                                                                                                                                   ProDom; PD000010; Homeobox; SMART; SM00389; HOX; 1.
                                                                                                                                         PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                      Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                 InterPro; IPR000047; HTH_repressr.InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                            ZFIN; ZDB-GENE-990415-120; hoxd3a.
                                                                                                                                                                                                                                                                                                           EMBL; Y13948; CAA74286.1; -. TRANSFAC; T03651; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prince V.E., Moens C.B., Kimmel C.B!, Ho R.K.;

"Zebrafish hox genes: expression in the hindbrain region of wild-type "Zebrafish hox genes: expression in the hindbrain region of wild-type and mutants of the segmentation gene, valentino.";

Submitted (JUN-1997) to the EMBL/GehBank/DDBJ databases.

-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyprinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio)
Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HXD3_BRARE
O42370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homeobox protein Hox-D3 (Fragment) HOXD3 OR HOXD3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00050; RIBOSOMAL_L23; 1, Ribosomal protein; rRNA-binding. SEQUENCE 164 AA; 18170 MW; 1606
1 SYDA 4
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                                       Similarity 4; Conser
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167
167
                                   100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                    HOMEOBOX_1;
                                                                                          18339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rRNA-binding.
18170 MW; 1606F4E8BFCE0C8F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation
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                                      0;
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                                                                                                                   HOMEOBOX.
                                                  Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB Pred! No. 1.3
                                                                                        E90327377FF865CF CRC64;
                                    Mismatches
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                                               1.4e+02;
                                                             DB 1;
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                                                            Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 164;
                                    Indels
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tions on its
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Best Local
                                                                                                          Q04450;
01-0CT-1994 (Rel. 30, Createa)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1990 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ribulose bisphosphate carboxylase small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCYD_ASPFU
O14434;
                                                                                                                                                                                    RBS2_MESCR ST/
Q04450;
01-OCT-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Aspergillus fumigatus arp1 modúlates conidial pigmentation and complement deposition.";
MOI. Microbiol. 26:175-183(1997).
-I- FUNCTION: MODULATES THE BLUISH-GREEN PIGMENTATION OF CONIDIA WELL AS COMPLEMENT DEPOSITION.
-I- CATALYTIC ACTIVITY: Scytalone = 1,3,8-tr1hydroxynaphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASPFU
                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004235; Scytalone_DH
Pfam; PF02982; Scytalone_DH; 1.
Lyase; Conidiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U95042; AAC49843.1; -. HSSP; P56221; 3STD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98043547; PubMed=9383199;
Tsai H.-F., Washburn R.G., Chang Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5085;
            SEQUENCE FROM N.A.
                                                                                                 Mesembryanthemum crystallinum (Common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable scytalone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus fumigatus (Sartorya fumigata).
 MEDLINE-93302719;
                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                      1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: BIOSYNTHESIS OF FUNGAL BLUISH-GREEN PIGMENT. DEVELOPMENTAL STAGE: EXPRESSED DURING CONIDIATION.
                                                                                                                                                                                                                                                                                          SYDA 31
                                                                                                                                                                                                                                                                                                                                                                                                       168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                       Caryophyllales;
 PubMed=8316216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dehydratase (EC 4.2.1.94).
                                                                                                                                                                                                                                                                                                                                                                                                         19716 MW;
                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 1;
Pred. No. 1.4e+02;
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                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         F40C22CEB6D02695 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                     180
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                                                                                                 plant)
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                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                           Length 168;
                                                                                                                                          chloroplast precursor
                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local S
Matches 4
                                                                     RBS1_MESCR STANDARD; PRT; 182 AA. Pp16032; 01-APR-1990 (Rel. 14, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Ribulose bisphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO small subunit 1). RBCS-1 OR RBCS OR RBCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luxaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae: Mesembruna: NCBI_TaxID=3544;
                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00101; RuBisCo_small; 1. PRINTS; PR00152; RUBISCOSMALL. ProDom; PD000290; RuBisCO_small;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L10214; AAA03694.1; -.
EMBL; M38316; AAA33036.1; -.
PIR; S35246; S35246.
InterPro; IPR000894; RuBisCO_small.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derocher E.J., Quigley F., Mache R., Bohnert H.J.; "The six genes of the Rubisco small subunit multigene family Mesembryanthemum crystalliqum, a facultative CAM plant."; Mol. Gen. Genet. 239:450-462(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crystallinum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carboxylase/oxygenase small subunit gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Derocher E.J., Michalowski C.B., Bohnert H.J.; "cDNA sequences for transcripts of the ribulose-1,5-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                      yase; Oxidoreductase; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photosynthesis; Carbon dioxide fixation; Photorespiration;
                                                                                                                                                                                                                                                    177 SYDA 180
                                                                                                                                                                                                                                                                               1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phospho-D-glycerate.

CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2)
3-phospho-D-glycerate + 2-phosphoglycolate.

SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.

SUBCELLULAR LOCATION: Chloroplast.

SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2
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                                                                                                                                                                                                                                                                                                                                                                   154
180 /
                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative 0
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20084 MW;
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T -> I (
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Pred. No.
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6977DC72C89940F3 CRC64;
                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast;
                                                                                                                                                                                                                                                                                                                        ; DB 1;
. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                     Length 180;
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                                                                                                      chloroplast precursor
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                                              Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
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ATPD_BACHD
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Best Local (
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                    ATPD_BACHD Q9K6H2;
Q9K6H2;
16-OCT-2001 (Re
16-OCT-2001 (Re
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ATP synthase de
ATPH OR BH3757.
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CONFLICT
SEQUENCE
  Bacillus
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PIR; S35247; S35247.
InterPro; IFR000894; RuBisCO small.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                               179 SYDA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photosynthesis; Carbon
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"The six genes of the Rubisco small subunit multigene family Mesembryanthemum crystallinum, a facultative CAM plant.";
Mol. Gen. Genet. 239:450-462(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesembryanthemum crystallinum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Derocher E.J., Ramage
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CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2)
3-phospho-D-glycerate + 2-phosphoglycolate.
SUBCHIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
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FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNCHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS, BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
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CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) =
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145
182 /
                           (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update
e delta chain (EC 3.6.3.14).
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                                                                                                                                              STANDARD;
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RuBisCO_small; 1.
'arbon dioxide fixation; Photoresparbon dioxide fixation; Photor
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182
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Pred. No. 1.5e+02;
""ematches 0;
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desert
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MEDLINE-3302719; PubMed=8316216; |
Derocher E.J., Quigley F., Mache R., Bohnert H.J.;
"The six genes of the Rubisco small subunit multigene family Mesembryanthemum crystallinum, a facultative CAM plant.";
Mol. Gen. Genet. 239:450-462(1993). |
                                                                                                                                                                                                 RB33_MESCR STANDARD; PRT; 183 AA. 008183; 01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 30, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Ribulose bisphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO small subunit 3).
                                                                                                                            Mesembryanthemum crystallinum (Common ice plant)
Eukaryota; Viridiplantae; Streptophyta; Embryoph
Spermatophyta; Magnoliophyta; eudicotyledons; coi
Caryophyllidae; Caryophyllales; Alzoaceae; Mesemi
                                                                                                                                                                                                                                                                                                                          MESCR
                                                                                          SEQUENCE
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TIGREAMS; TIGRO1145; ATP_synt_deltd; 1.
PROSITE; PS00389; ATPASE_DELTA; 1.
Hydrolase; ATP synthesis; CF(1); Hydrog-
Complete proteome.
SEQUENCE 183 AA; 20605 MW; 5CB7989A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not|removed entities requires a license agreement (See lor send an email to licenseeisb-sib.ch).
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Pfam; PF00213; OSCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP001519; BAB07476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the alkaliphilic bacterium Bacill halodurans and genomic sequence comparison with Bacillus subti Nucleic Acids Res. 28:4317-4331(200);
-i- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT CF(0) TO CF(1). IT EITHER TRANSMITS CONFORMATIONAL CHANCES CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20512582; PubMed=11058132; Takami H., Nakasone K., Takaki Y., Maeno G., S. Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                 101 SYDA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; NCBI_TaxID=86665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), CAMMA(1), DELTA(1), EPSILON(1). CF(1) HAS THREE MAIN SUBUNITS: A, B AND C.

SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) =
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                                                                                     FROM N.A.
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                                                                                                                                          Streptophyta; Embryophyta; yta; eudicotyledons; core eu
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 1;
Pred., No. 1.5e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5CB7989AFA5D26F2 CRC64;
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                                                                                                                          Mesembryanthemum
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V., Kuhara S.
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                                                                                                                                            eudicots;
                                                                                                                                                         Tracheophyta;
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Derocher E.J., Michalowski C.B., Bohnert H.J.;

Derocher E.J., Michalowski C.B., Bohnert H.J.;

"CDNA sequences for transcripts of the ribulose-1,5-bisphosphate

"carboxylase/oxygenase small subunit gene family of Mesembryanthemum

crystallinum.";

Plant Physiol. 95:976-978(1991).

-I-FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF

D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC

CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF

THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH

REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME

ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE
                                                                                                                                                                                                                                                                                                          RBS6_MESCR STANDARD; PRT; 186 AA. 008186; 01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 30, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Ribulose bisphosphate carboxylase small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000894; RuBisCO_small: Pfam; PF00101; RuBisCO_small; 1. PRINTS; PR00152; RUBISCOSMALL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00152; I
ProDom; PD000290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L10215; AAA03695.1;
EMBL; M38317; AAA33037.1;
PIR; S35245; S35245.
                    SEQUENCE FROM N.A. MEDLINE=93302719; PubMed=8316216;
                                                                                                                                      Mesembryanthemum crystallinum (Common ice plant).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Photosynthesis; Carbon dioxide fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lyase; Oxidoreductase; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 SYDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate phospho-D-glycerate.
CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Chloroplast. SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-phospho-D-glycerate + 2-phosphoglycolate.
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
                                                                                                                                                                                                                                                                                  4.1.1.39)
E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                  (RuBisCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
Quigley F., Mache R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RuBisCO_small; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
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M -> I (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHLOROPLAST (BY SIMILARITY).
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> I (IN REF. 2).
F056AAA5B110AA71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
No.
Bohnert H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5e+02;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Photorespiration;
                                                                                                                                                                                                                                                                                                          6, chloroplast precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
     obtained by genetic Proc. Natl. Acad. So -!- FUNCTION: Destro
                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=CV. P2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000894; RuBisCO_small.
Pfam; PF00101; RuBisCO_small; 1.
PRINTS; PR00152; RUBISCOSMALL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The six genes of the Rubisco small subunit multigene family from Mesembryanthemum crystallinum, a facultative CAM plant.";
Mol. Gen. Genet. 239:450-462(1993).
-i- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryop
Spermatophyta; Magnoliophyta; eudicotyledons; c
Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (Rel. 19,
01-AUG-1991 (Rel. 19,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyase; Oxidoreductase; Monooxygenase; Multigene family.
TRANSIT 1 61 CHLOROPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L10213; AAA03698.1; -. PIR; S35242; S35242.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=4092;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SODB
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superoxide dismutase [Fe],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000290; RuBisCO_small; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                              van Camp W.,
                                                                                                                                                                      MEDLINE=91088619; PubMed=2263641;
                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SODF_NICPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                    "Characterization of iron superoxide dismutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 SYDA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SYDA 4
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CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate
3-phospho-D-glycerate + 2-phosphoglycolate.
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative
                                                                                                                                           Bowler C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
enetic complementation in Escherichia coli.", cad. Sci. U.S.A. 87:9903-9907(1990).
Destroys radicals which are normally produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
[Fe], chloroplast (EC 1.15.1.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                           Villarroel R., Tsang E.W.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBULOSE BISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5825DFF86F86B7F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5e+02;
                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta; dons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                          cDNAs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                              Montagu
                                                                                       plants
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        within
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RESULT 20 FLID_PROMI
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                   FLID_PROMI P42274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
or send a
                  "Sequence and genetic analysis of multiple flagellin-encoding of the proteus mirabilis.";

Gene 148:33-41(1994).

-i- FUNCTION: REQUIRED FOR THE MORPHOGENESIS AND FOR THE ELONG. THE FLAGELLIN MONOMERS AT THE TIP OF GROWING FILAMENT. FORMS A STRUCTURE, WHICH PREVENTS FLAGELLIN SUBUNITS (TRANSPORTED THE CENTRAL CHANNEL OF THE FLAGELLUM) FROM LEAKING OUT WITH DOLYMERIZATION AT THE DISTAL END (BY SIMILARITY).

-i- SUBUNIT: HOMOPENTAMER (BY SIMILARITY).

-i- SUBUNIT: HOMOPENTAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Flagellar hook-associated protein 2 (HAP2) (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pfam; pF00081; sodfe_C; 1.
pfam; pF02777; sodfe_C; 1.
proDom; pD000475; SODismutase; 1.
proSITE; pS00088; SOD_NN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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        - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A39267
HSSP; P0915
                                                                                                                                                      Belas R., Flaherty D.;
                                                                                                                                                                              STRAIN-BB2000
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Proteus
                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                 FLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS0008
Ox1doreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M55909; AAA34074.1; -.
                                                                                                                                                                 MEDLINE-95011656; PubMed-7926835;
                                                                                                                                                                                                                                                   Proteus mirabilis
                                                                                                                                                                                                                                                                         (Flagellar cap protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001189; SODismutase.
                                                                                                                                                                                                               NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                          107 SYDA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2). COPACTOR: Iron.
SUBGUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Chloroplast.
INDUCTION: BY ENVIRONMENTAL CONDITIONS.
SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P09157; A39267.
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78
162
166
202
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                 STANDARD;
           BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iron;
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26 I
78 I
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23042 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast.
           TO THE FLID FAMILY.
                                                                                                                                                                                                                                      gamma subdivision; Enterobacteriaceae;
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RESULT 21
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P45503;
01-NOV-1995
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entities
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30-MAY-2000
Cell divisio
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between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                        MEDLINE=94374704; PubMed=8088545; bharmatilake A.J., Kendrick K.E.; "Expression of the division-controlling gene ftsz during growth sporulation of the filamentous bacterium Streptomyces griseus."; Gene 147:21-28(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flagella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               EMBL;
                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces
Bacteria; Act
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales;
NCBI_TaxID=1911;
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    -!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
    -!- SIMILARITY: BELONGS TO THE FTSQ FAMILY.

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153 SYDA
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                                                                                                                                    division;
                                                                                                                                                 U07344; AAA56888.1;
                                                                                                                                                                       non-profit institutions as long and this statement is not removed. s requires a license agreement (See lan email to license@isb-sib.ch).
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                                                          Similarity
156
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Actinobacteria; Actinobacteria (class); Actinobacteridae;
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205 AA;
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(Rel. 32,
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on protein
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                                                                                               AA;
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ftsQ homolog (Fragment).
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6E82 CRC64;
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HXB3_BRARE
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                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                           DNA_BIND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prince V.E., Moens C.B., Kimmel C.B., Ho R.K.; "Zebrafish hox genes: expression in the hindbrain region of wild-type and mutants of the segmentation gene, valentino."; Development 125:393-406(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertactinopterygii; Neopterygii; Teleostei; Ostacyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HXB3_BRARE STANDARD; PRT; 210 AA 042368; 15-JUL-1999 (Rel. 38, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat HOMEODOX protein HOX-B3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00024; HOMEOBOX. PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000010; Homeobox; 1. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZFIN; ZDB-GENE-990415-104; hoxb3a.
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                                                                                                                                                                                                                                                                                    Transcription regulation.
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InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98165394; PubMed-9425135;
                                                                                                                                                                                                                                                                                                                                                Homeobox;
69
                                                                                                            Local Similarity es 4; Conserv
                                                1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
FUNCTION: SEQUENCE-SPECIFIC TRANSPORT DESCROOK WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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SUBCELLULAR LOCATION: Nuclear.
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SYDA 72
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22862 MW;
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Pred. No. 1.7
0; Mismatches
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Ostariophysi; Cypriniformes;
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Na GM.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Ballga N.S., Thorsson V., Sbrogna J.,

A Shukla H.D., Lasky S.R., Ballga N.S., Thorsson V., Sbrogna J.,

A Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

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A Leithauser B., Keller R., Goo Y.A.,

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A Leithauser B., Keller B., Goo W., J., Hough B., Leithauser B., Goo Y.A.,

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A Leithauser B., Keller B., Goo Y.A.,

A Leithauser B., Leithauser B., Goo Y.A.,

A Leithauser B., Keller B., Goo W., J., Hough B., Louder B., Goo Y.A.,

A Leithauser B., Keller B., Goo M., J., Hough B., Louder B., Goo M., J., Hough B., Lou
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p57687;
p57687;
p57687;
p57687;
p670687;
p670687;
p670687;
p67087;
p67
                                                           OLII_HUMAN STANDARD; PRT; 216 AA. P47889; P47889; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) O1factory receptor-like protein OR17-207 (Fragment).
                                                                                                                                                                                                                                                                                         _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE005153; AAG20845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=64091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Membrane-associated (Probable). SIMILARITY: BELONGS TO THE KDPC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K(+)(In).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003820; K_ATPase_KdpC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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23768 MW;
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Pred. No. 1.8e+02;
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Best Local
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                                                                                                                                                                                                                                                                                    U119_CAEBR
Q17297;
Q1-NOV-1997
                                                                                                                                                                                                           Unc-119
UNC-119.
SEQUENCE FROM N.A.

MEDLINE-97149282; PubMed-8996090;

Maduro M.F., Pilgrim D.B.;

"Conservation of function and expression of unc-119 from two
Caenorhabditis species despite divergence of non-coding DNA.";
                                                                                                                                                                                                                                                                                                                                                   CAEBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
                                                                                                                                                Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                    Caenorhabditis briggsae.
                                                                                                                                                                                                                                               01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-protein
Multigene
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Ben-Arie N., Lancet D., Taylor C.,
Ledbetter D.H., Carrozzo R., Patel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Olfactory receptor gene cluster on human duplication of an ancestral receptor reper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              North M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-94272458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lication of an ancestral receptor rep. Mol. Genet. 3:229-235(1994).
FUNCTION: PUTATIVE ODORANT RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions how non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                            SYDA
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                                                                                                                                                                                                                           protein.
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(Rel.
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                                                                                                                                                                                                                                               . 35, Created)
. 35, Last sequ.
. 40, Last anno
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G_PROTEIN_RECEP_F1_2;
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                                                                                                                                                                  Nematoda; Chromadorea;
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Last annotation updat
                                                                                                                                                Caenorhabditis
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CYTOPLASMIC (PC
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5 (POTENTIAL)
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Pred. No. 1.8
); Mismatches
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3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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K., S
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Sheer D., Lehrach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8e+02;
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                                                                                                                                                                Rhabditida; Rhabditoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
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RESULT 26
U119_CABELL
U119_CAB
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_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unc-119 protein.
UNC-119 OR M142.1
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                        WormPep; M142.
Developmental
                                                                EMBL; U32854; AAC46919.1; -. EMBL; 273428; CAA97807.1; -.
                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                           modified
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maduro M.F., Pilgrim D.B.;
"Identification and cloning of unc-119
Caenorhabditis elegans nervous system.
Genetics 141:977-988(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=96129273; PubMed=8582641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
[1]
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01-OCT-1996 (Rel.
16-OCT-2001 (Rel.
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01-0CT-1996
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                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                             McMurray A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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FUNCTION: REOUTRE
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                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE PDE6D
                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                 NERVOUS SYSTEM.
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4; Conserv
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                                                                                                                                                                                                                                              the Swiss Institute
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                                              1; CE06203.
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34, Last seg
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26F43457C5CDEB45 CRC64;

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YPVA_METTF
ID YPVA_METTF
AC P29577;
AC P29577;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence of the control of the
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Y945_METJA
Q58355;
01-NOV-1997
01-NOV-1997
16-OCT-2001
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MEDLINE-96377999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Manna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was used.
              Plasmid pFV1.

Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 21 41 POTENTIAL. SEQUENCE 224 AA; 25416 MW; 1E9FF7E32C025DA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U67538; AAB98955.1; TIGR; MJ0945; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jannaschii.";
Science 273:1058-1073(1996).
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Last annotation updat
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Pred. No. 1.8e+02;
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Pred. No. 1.9e+02;
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RESULT 29
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AC P05357;
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Best Local S
Matches 4
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01-AUG-1991 (Rel. 19, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                      the European Bioinformatics Institute. There are no rest use by non-profit institutions as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                This
                                                                                                                                                                                          "Analysis of the complete nucleotide sequence of tumefaciens virB operon."; nucleic Acids Res. 16:4621-4636(1988).
-i- FUNCTION: VIRB PROTEINS ARE SUGGESTED TO ACT
                                                                                                                                                                                                                                                      MEDLINE=88247765; PubMed=2837739;
Thompson D.V., Melchers L.S., Idler K.B.,
Hooykaas P.J.J.;
                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens Plasmid pTi15955. Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                            VIRB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01345; DUF11; 1.
Hypothetical protein; Plasmid.
SEQUENCE 227 AA; 24681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X68366; CAA48429.1; PIR; S26440; S26440. PIR; S30305; S30305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93126090; PubMed=1336177;
Noelling J., van Eeden F.J.M., Eggen R.I.L., de Vos W.M.;
Modular organization of related Archaeal plasmids encoding
restriction-modification systems in Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-DSM 3848 / THF;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                          VirB8 protein
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Nucleic Acids Res.
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                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=190386
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                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                               alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                             (strain 15955).
                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Pred. No.
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ROLE
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hes 0;
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                                                                                                                                                                                                                                                                      Shilpercort R.A.,
                                                                                                                                                                             ACT AT THE BACTERIAL IN DIRECTING T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 227;
                                                                                                                                                                                                                                         the Agrobacterium
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for
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EMBL; X06826; CAC15165.1;

ALT_INIT

(See http://www.isb-sib.

.ch/announce/

S00784; B8AG55

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RESULT 31
Y416_CHLTR
ID Y416_C:
AC 084421
DT 16-OCT
DT 16-OCT
DT 16-OCT
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VIB8_AGRTU
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084421;
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                                                                                                                                                                                                 Crown gall
                                                                                                                                                                                                                      EMBL; J03216; -; NOT_ANNOTATED_CDS PIR; I28621; B8AGA6.
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P09781;
                                                                                                        104
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             Ward J.E.,
Nester E.W.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90170994; PubMed=2307685;
Ward J.E., Akiyoshi D.E., Regier D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                               tumefaciens Ti plasmid.";
tumefaciens Ti plasmid.";
T. Biol. Chem. 263:5804-5814(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of the virB operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ward J.E., Akiyoshi D.
Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88186901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agrobacterium
Plasmid pTiA6
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SEQUENCE
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                                                                                                                               1 SYDA 4
                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 265:4768-4768(1990).
- FUNCTION: VIRB PROTEINS ARE SUGGESTED TO SURFACE AND THERE PLAY AN IMPORTANT ROLE TRANSFER TO PLANT CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                               tumor; Plasmid.
230 AA; 25382 MW;
  (Rel. 40, Created)
(Rel. 40, Last sequence)
(Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor; Plasmid.
230 AA; 25408 MW;
                                                                                                                                                    Conservative
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                                                STANDARD;
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hi D.E., Regier
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Last sequence update)
Last annotation updat
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                                             PRT;
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Pred. No.
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Pred. No.
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hes 0;
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                                                                                                                                                                      Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                      Gordon
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RESULT 32
VIB8_AGRT5
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Matches
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P17798;
01-AUG-1990
01-NOV-1990
15-JUN-2002
                                                                                MEDILINE=90318324; pubMed=2370849;
Kuldau G.A., de Vos G., Owen J., N
"The virB operon of Agrobacterium
reading frames.";
                                                                                                                                                                                                                            Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                     Agrobacterium tumefaciens Plasmid pTiC58.
                                                                                                                                                                                                                                                                                                        VirB8 protein.
VIRB8 OR ATU6174 OR AGR_PTI_11.
SEQUENCE FROM N.A. MEDLINE-90301800;
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                          NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00382; AAA; 1
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InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of an obligate infracellular pathogen of humans: Chlamydia trachomatis.",
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stephens R.S., Kalman S., I
Mitchell W.P., Olinger L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis. Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable metal transport system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                             Gen.
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FOR A METAL. PROBABLY RESPONSIBLE FOR ENER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                          Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AA;
                                                                                                                                                                                                                                                                                                                                                 (Rel. 15, Created)
(Rel. 16, Last seq.
(Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                    221:256-266(1990)
                                                                                                                                         PubMed=2370849;
PubMed=2194232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
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                                                                                                                                                                                                                                                                                                                                                 Last annotation
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                                                                                                                                                                                                                                             alpha subdivision; Rhizobiaceae
                                                                                                                                                                                                                                                                                      (strain C58 / ATCC
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                                                                                                                                                                                                                                                                                                                                                                         sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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; DE74774507950365 CRC64;
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Pred. No.
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                                                                                                  tumefaciens
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G.,
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ENERGY COUPLING TO THE
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oTiC58 encodes
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
                                                                                                  SCHGR
                                                                                                                                                                                                                                                                                                                                                               EMBL; X53264; CAA37361.1; -.
EMBL; J03320; AAA91598.1; -.
EMBL; AE009436; AAL46410.1; -.
EMBL; AE007923; AAK90936.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001)
                                                                  PBCB_SCHGR
P82886;
                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumefaciens: complete nucleotide sequence and gene
the 28.63-kbp regulon cloned as a single unit.";
plasmid 23:85-106(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROGOWSKY P.M., POWell B.S., Shirasu K., Lin T.-S., Morel P., Zyprian E.M., Steck T.R., Kado C.I., "Molecular characterization of the vir regulon of Agrobacterium "Molecular characterization of the vir regulon of Agrobacterium"
        Putative
                      16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21608551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21608550; PubMed-11743193;
                                                     16-OCT-2001
                                                                                                                                                                111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                            1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: VIRB PROTEINS ARE SUGGESTED TO SURFACE AND THERE PLAY AN IMPORTANT ROLE TRANSFER TO PLANT CELLS.
                                                                                                                                                              |||||
| SYDA 114
                                                                                                                                                                                                                                                                                                                                                    S12348; B8AG58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ε.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W., Setubal J.C., Kaul
                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294:2317-2323(2001).
      beta-carotene
                                                                                                                                                                                                                                                                                        128
237
                                                                                                                                                                                                                                                                                                                                  tumor; Plasmid;
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat-
ta-carotene binding protein.
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                        AA;
                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                     22 M
129 S
; 26294 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     natural genetic
                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                 Complete proteome
                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                   MISSING
SA -> TR
                                                                                                                                                                                                                                         Score 21;
Pred. No.
                                                                                  PRT;
                                                                                                                                                                                                                                                                                     ISSING (IN REF. 1).
A -> TR (IN REF. 2)
71FEE1084B9597E9 C
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monks D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     engineer Agrobacterium tumefaciens
                                                                                  250
                   update)
                                                                                                                                                                                                                                         2e+02;
                                                                                  ₿
                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT AT THE BACTERIAL IN DIRECTING T-DNA
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kitajima
                                                                                                                                                                                                                                                        Length 237;
                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in no way
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: ;
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Y625_TREPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                         MEDINIE-98332770; PubMed=9665876;
MEDINIE-98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
Khalak H., Richardson D., Bowman C., Cotton M.D., Fujii C., Garland S
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S
McDonald L., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Purification and sequence determination of a yellow protein from sexually mature males of the desert locust, Schistocerca gregaria. Insect Biochem. Mol. Biol. 31:1183-1189(2001).

-!- FUNCTION: Has beta-carotene-binding activity. May be involved the transport of carotenes from internal tissues to epidermis cuticle of the locust.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schistocerca gregaria (Desert locust).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; (Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
                                                                                     entitles requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                   spirochete.";
Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Nichols;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O83633;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y625_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wybrandt G.B., Andersen S.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Cuticle; PubMed=11583931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=160;
                                                                                                                                                                                                                                              "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                     /enter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 SYDA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: Deposited in the epidermis and cuticle locusts during their sexual maturation. erPro; IPR004272; Odorant_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat)
protein TP0625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUF233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25666 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6074CF88D822EB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                    restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gregaria.";
                                                                                                                                                                      EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hexapoda;
Caelifera;
                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                                                                                               Garland S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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EMBL; AE001237; AAC65604.1; TIGR; TP0625; -.

Hypothetical protein; DOMAIN 165 20

28874 MW;

Coiled

coil; Complete proteome.
COILED COIL (POTENTIAL).
; 107002FE47B25186 CRC64;

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В
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Lather S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Goliver K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Gulberford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RT German S., Sanchez G., Ra Three Genes Fon Datashkin J.,
RA Challer H., Wambutt R., Paulsen I., Potashkin J.,
RA Challer H., Wamb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 35
RL7C_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the B
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                              Pfam; PF00327; Ribosomal_L30; 1.
TIGRFAMS; TIGR01310; L7; 1.
PROSITE; PS00634; RIBOSOMAL_L30; 1.
                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                    EMBL; AL022304; CAA18409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60S ribosomal protein L7-C. RPL7C OR SPBC18H10.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYDA
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                                                                                                                                                                     IPR000517; Ribosomal_L30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
protein; Multigene
251 AA; 28730 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0
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                                  family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 1;
Pred. No. 2.1e+02;
   5382A27E39F3800E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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on update)
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                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                               There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                       Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL
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MBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                       outstation
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RESULT 36
SOJ_TREPA
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                                                                                                                                     RESULT 37
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Best Local (
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                             BIOC_SERMA STANDAKU,
P36571;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                       NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOJ_TREPA
083296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Dodson R., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Sodergren E., Hardham J.M., McLeod M.P., Salzberg M., Utterback T., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weldman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foe entitles requires a license agreement (See http://www.isb-slb.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                             InterPro; IPR000707;
Pfam; PF00991; ParA;
                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001208; AAC65260.1; -. TIGR; TP0272; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence spirochete.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
               Serratia marcescens
                                                                                                                                                                                                                                                                                                               ATP-binding; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hatch B., Horst K.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98332770; PubMed=9665876;
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                                                                                                                                                                               228 SYDA 231
                                                                                                                                                                                             1 SYDA 4
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Proteobacteria; gamma subdivision;
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253 ‡
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17 AT
27341 MW;
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                                                                                                                                                                                                                                              Score 21; DB 1;
Pred. No. 2.1e+02;
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Pred. No. 2.1e+02;
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                                                     update)
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  Enterobacteriaceae;
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                                                                                                                                                                                                                                   Indels
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P077630;
P077630;
P077630;
P07-2001 (Rel. 10, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase II (EC 4.2.1.1) (Carbonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           Mezquita J., Pau M., Mezquita C.;

"A novel carbonic anhydrase II mRNA isolated from mature chicken testis displays a TATA box and other promoter sequences in a leady untranslated region not present in somatic tissues.";

Gene 147:231-235(1994).
SEQUENCE OF 4-259 FROM N.A. STRAIN-White leghorn; TISSUE-Retina:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Hubbard White Mountain; TI MEDLINE-95011620; PubMed-7926806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHICK
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11- EUNCTION: BIOC IS INVOLVED IN AN EARLY, BUT CHEMICALLY UNEXPLORED,
STEP IN THE CONVERSION OF PIMELIC ACID TO BIOTIN.
-1- PATHWAY: Biotin biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain.
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                                                                                                                                                                                            STRAIN=White leghorn;
MEDLINE=87146391; PubMed=3029691;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archosauria; Aves;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01209; Ubie_methyltran;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000051; SAM_bind.
InterPro; IPR004033; UbiE/COQ5_Metrf.
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                                                                                                                                     Yoshihara C.M., Lee J.-D., Dodgson J.B., "The chicken carbonic anhydrase II gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakurai N., Imai Y., Masuda M., Komatsubara S., Molecular breeding of a biotin-hyperproducing
                                                                                                                 in intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYDA
                                                                                    on position.";
Acids Res. 15:753-770(1987).
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X17378; CAA35250.1; -
EMBL; M25943; AAA48646.1; -
PIR; S01078; S01078.
PIR; A26415; A26415.
PIR; S10229; S10229.
PIR; S10229; S10229.
PIR; S31987; S31987.
                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90192090; PubMed-1969140; Godbout R., Andison R., Upton C., Day R.; "Utilization of the second polyadenylation the chicken carbonic anhydrase II gene."; Nucleic Acids Res. 18:1049-1049(1990).
                                                                                                                                                                                                                                                                                              METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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"Isolation of the chicken carbonic anhydrase II gene.";
Ann. N.Y. Acad. Sci. 429:332-334(1984).
-i- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-i- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Lyase; Z
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00194; carb_anhydrase; ProDom; PD000865; Euk_COanhd; 1
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                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
  49
                                         1 SYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS
SYDA
                                                                                                      Similarity
  52
                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001148; Euk_COanhd
                                                                                                                                                                    259 AA;
                                                                                                                                                                                                                                   0
93
95
118
17
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                               EUK_CO2_ANHYDRASE;
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93
118
118
7
86
249
                                                                                                                                                                    28876
                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
JOINED.
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ZINC (CATALYTIC).
ZINC (CATALYTIC).

V -> L (IN REF. 3).
V -> S (IN REF. 5).
V -> V (IN REF. 2).
                                                                                   0
                                                                                                      Score 21;
Pred. No.
                                                                                                                                                                      DF133083864A4969
                                                                                     Mismatches
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                                                                                   2.2e+02;
hes 0;
                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
                                                                                                                        Length 259
                                                                                                                                                                      CRC64;
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RESULT

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Mayer M. S. X., Schueller C. Wambutt R., Murphy G., Volckert G. Ra Poll T., Dusterhoeft A., Stiekena W., Entlan K.-D., Terryn N., Ra Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Ra Welchselgartner M., de Simone V., Obermaier B., Mache R., Wheller R. Ra Kreis M., Delseny W., Pulgdomenech P., Watson M., Schmidtheini T. Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Ra Reichert B., Rosee M., Hauf J., Koetter P., Ra Reichert B., Pardit A., Peters S., Van Staveren M., Dirkse W., Ra Rolonsom S., Hauf J., Rose M., Hauf J., Koetter P., Ra Bernelser S., Hampel S., Feldpausch M., Lennard N., Wallen S., Van den Daele H., Ra Van Montagu M., Rogers J., Cronin A., Quali M., Bray-Allen S., Van Montagu M., Rogers J., Cronin A., Quali M., Bray-Allen S., Ra Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Rettett A., Rajandream M.A., Lyne M., Benes V., Rochmann S., Avglition A., Vitale D., Liquori R., Macher S., Ra Borkova D., Bloecker H., Scharfe M., Granderath K., Danner D., Herril A., Ra Ra Reicher S., Perimann B., Granderath K., Danner D., Herril A., Scharfe M., Graver S., Scholler P., Heber S., Francs P., Bielke C., Ra Schons S., Tacon D., Jesse T., Ra Gleber J., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., Ra Gleber J., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., Ra Gleber J., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., Ra Gleber J., Berth J., Roches M., Aburtheideh J., Ra Littelle P., Couche M., Aburtheideh J., Ra 
Q9SVE5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Expansin-like 2 precursor (At-EXPL2) (Ath-ExpBeta-2.2)
EXPL2 OR AT4G38400 OR F22II3.IT0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _ARATH
                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
MEDLINE=20083488; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPL2 OR Aff4638400 on Livery or cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; Erassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                                                                             402:769-777(1999).
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RESULT 40
FLIP_CAUCR
ID FLIP_C
AC Q45980
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Best Local S
Matches 4
Nierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh
                                                                                                                                                                                                                                                                                                                         FLIP_CAUCR STANDARD; PKI; 4
Q45980; | 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                Caulobacter crescentus division.";
                                                                  MEDLINE=21173698;
Nierman W.C., Felo
                                                                                                                                              division.
                                                                                                                                                                                  Wingrove
                                                                                                                                                                                             Gober J.W.,
                                                                                                                                                                                                                        STRAIN-ATCC
                                                                                                         SEQUENCE
                                                                                                                                                                       "Temporal and
                                                                                                                                                                                                        MEDLINE=95325304; PubMed=7601828;
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                      Flagellar biosynthetic
                                                                                                                                                                                                                                                            NCBI_TaxID=155892;
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PRODOM; PD002179; PO11en_allergen; 1.

PROSITE; PS50843; EXPANSIN_EG45; 1.

PROSITE; PS50842; EXPANSIN_EG45; 1.

Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL035539; CAB37496.1;
EMBL; AL161593; CAB80505.1;
EMBL; AY050470; AAK91483.1;
EMBL; AF378855; AAK55658.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                 Bacteriol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DATABASE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                       FROM
                                                                                                                                                                                                                    FROM N.A.
TCC 19089 /
                                                                                                                                                                                  J.A.
                                                                                                                                                                                              Boyd C.H., Jarvis M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 AA;
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22
42
162
100
103
                                                                                                                              177:3656-3667(1995).
                                                                                                                                                      spatial regulation of flip, an rescentus that is required for m
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265
148
244
200
100
103
28642
                                                                             PubMed=11259647;
                                                                                            / CB15;
                                                                                                                                                                                                                       CB15;
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                                                                                                                                                                                                                                                                                                                      protein
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EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
M; B57B4C921899F40D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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EXPANSIN-LIKE :
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                                                                                                                                                                                                                                                                                                                       flip
                                                                                                                                                                                                                                                                                 subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                         Mangan E.K., Rizzo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                  266
                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                      n early flagellar motility and norm
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                                                                                                                                                                                                                                                                             Caulobacter group;
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                                                              Nelson K.E.,
                                                                                                                                                      normal cell
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               Berry
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                                   Ely B.,
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Salzberg

S.L., Venter J.C.,

Shapiro L., Fraser C.

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PANB

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Best Local
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Q9X712;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flagella;
TRANSMEM
  "Complete
Submitted
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / DSM 20300 / NO
MEDLINE-99240418; PubMed-10223988;
                                                                                                                                                                                                                                                                                                                                                                                                                  (Ketopantoate hydroxymethyltransferase PANB OR CGL0114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum Bacteria; Actinobacteria; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc.
                                                               SEQUENCE FROM N.A. STRAIN-ATCC 13032
                                                                                                                                                  overproduction."
                                                                                                                                                                  "D-Pantothenate synthesis in Corynebacterium panBC and genes encoding L-valine synthesis i
                                                                                                                                                                                                                                                                                                                        Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OUN-2002 (Rel. 41, Last annotation updat)
3-methyl-2-oxobutanoate hydroxymethyltransf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                      Nakagawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Natl. Acad. Sci. U.S.A. 98:4136-4141(2001). FUNCTION: MAY BE A COMPONENT OF THE FLAGELLUM. NORMAL CELL DIVISION. MAY BE IMPLICATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EM
European Bioinformatics Institute. There are no resti
                                                                                                                              Environ. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
4; Conserv
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20 40
58 78
102 122
202 222
226 AA; 28527 1
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(MAY-2002) to
                  genomic sequence of Corynebacterium
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                                                                                                                                                                                                                   Sahm H.;
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FLIP_2; 1.
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the EMBL/GenBank/DDBJ
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Actinobacteria (class); Actin
cterineae; Corynebacteriaceae;
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glutamicum
databases.
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CYNT_SYNY3
C54735; P74088;
01-NOV-1997 (Rel. 35, Created)
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EMBL; AP005274; BAB97507.1; -.
InterPro; IPR003700; Pantoate_transf.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=97061201; PubMed=8905231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02548; Pantoate_transf; 1.
TIGRRAMS; TIGR00222; panB; 1.
Pantothenate blosynthesis; Transferase; Methyltransferase.
SEQUENCE 271 AA; 28552 MW; 0D5A8DCA903A03FA CRC64;
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                                                                                                                                                 FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE. ESSENTO PHOTOSYNTHETIC CARBON DIOXIDE FIXATION.
CAPALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
SIMILARITY: BELONGS TO THE PLANT AND PROKARYOTIC CARBONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
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PROSTTE; PS00704; PROK_CO2_ANHYDRASE_1; 1.

PROSTTE; PS00705; PROK_CO2_ANHYDRASE_2; 1.

LYase; Zinc; Complete proteome. L (IN RE CONFLICT 219 219 P -> L (IN RE CONFLICT 219 P -> L (IN RE CONFLICT 219 219 P -> L (IN RE CONFLICT 219 P -> L (IN RE CONFLI
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Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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STRAIN-Bristol N2;
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                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                   Hypothetical protein; Alternative splicing.
DOMAIN 2 64 ARG/SER-RICH.
DOMAIN 87 150 GLU-RICH.
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Deloughery C., Lee H.-M., DuBois J.,

A Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,

A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Qiu D.,

A Harrison D., Hoang L., Keagle P., Jumm W., Potthier B., Qiu D.,

A Harrison D., Hoang L., Keagle P., William W., Gibson R.,

A Jiwani N., Caruso A., Bush D., Safer H, Patwell D., Prabhakar S.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

Tomplete genome sequence of Methanobacterium thermoautotrophicum

"Complete genome sequence of Methanobacterium thermoautotrophicum

"Complete genome sequence of Methanobacterium thermoautotrophicum

"Complete Genome analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

J. Bacteriol. Phosphate.

C. Complete Methanobacterium thermoautotrophicum

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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Created)
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermopacter.
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-!- SIMILARITY: BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.
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Pfam; PF00459; inositol_P; 1.

PROSITE; PS00629; IMP_1; 1.

PROSITE; PS00630; IMP_2; 1.

PROSITE; PS00630; IMP_2; 1.

Hydrolase; Magnesium; Complete proteome.

Hydrolase; Magnesium; Complete Pf0AE435970AED882 CRC64;

SEQUENCE 280 AA; 30173 MW; F0AE435970AED882 CRC64;
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P32436;
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                      Bacillus subtilis.
Bacteria; Firmicutes;
NCBI_TaxID=1423;
MEDLINE=94018599; PubMed=8412657;
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Pred., No. 2.4e+02;
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RX MEDLINE-98044033; PubMed-9384377;

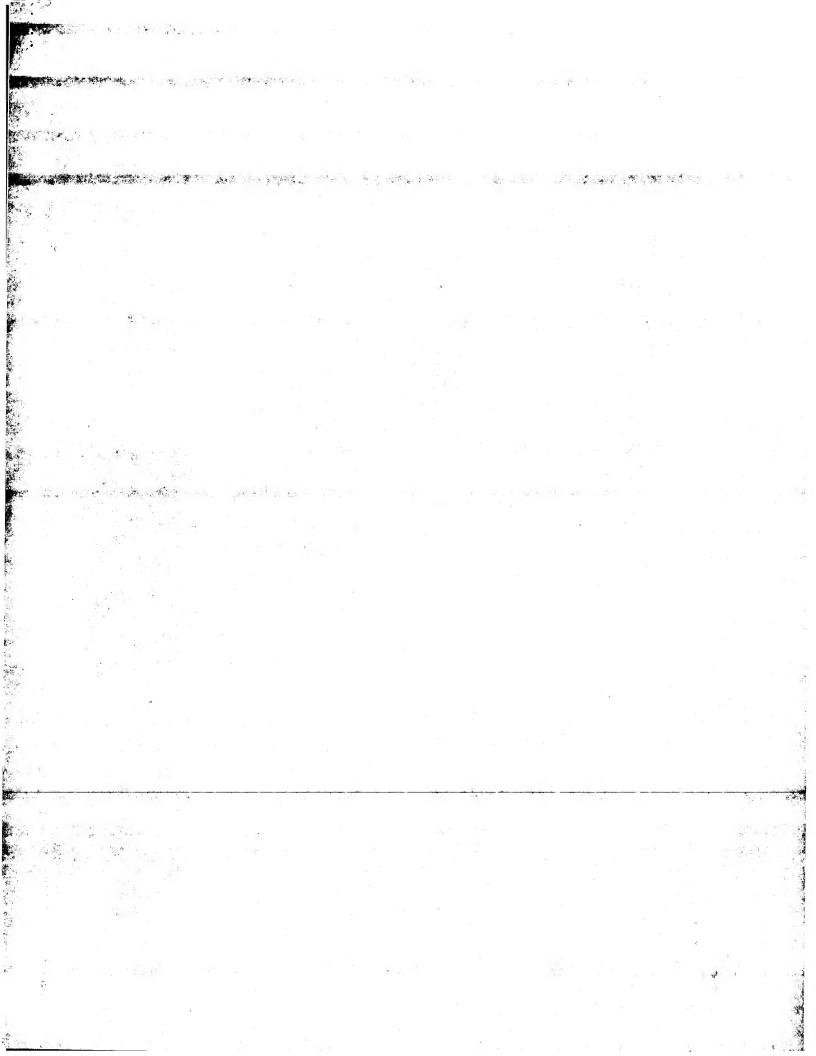
RX MEDLINE-98044033; PubMed-9384377;

RA Azevedo V., Bertero M.G., Messieres P., Bolotin A., Borchert S., RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bron S., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Borriss R., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D., RA Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Hilbert H., Holsappel S., Hosono S., Klaerr-Blanchard M., Klein C., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Ka Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Mediau C., Medigue C., RA Mediau C., Medigue C., RA Mediau C., Medigue C., RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Parro V., Pohl T.M., Schreich S., Schroeter R., Scoffone F., Sadaie Y., RA Perscant A., Tackeni E., Schleich S., Schroeter R., Scoffone F., San Takeuchi M., Tamakoshi A., Tanaka T., Tarkahashi H., Takemaru K., Parka Minters P., Wipat A., Yanamoto H., Yamane K., Yasamoto K., Yata Y., Yata Y.
                                                                                        EMBL; Z18629; CAA79225.1; -.
EMBL; U56901; AAC44939.1; -.
EMBL; 299122; CAB15565.1; -.
EMBL; M23558; -; NOT_ANNOTATED_CDS
PIR; D30191; D30191.
PIR; S28596; S28596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   component signalling systems.";
J. Bacteriol. 170:5102-5109(1988).
-i- SIMILARITY: TO S. AUREUS PLASMID PSK1 HYPOTHETICAL 15.5 kDa PROTEIN (AC P13977) AND TO M.GENITALIUM MG326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Henner D.J., Yang M., Ferrari E.;
"Localization of Bacillus subtilis sacU(Hy) mutations to two
genes with similarities to the conserved procaryotic family
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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"Sequence of the Bacillus
to 307 degree.";
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"comf, a Bacillus subtilis late competence locus, encodes a protein similar to ATP-dependent RNA/DNA helicases.";
Mol. Microbiol. 9:119-131(1993).
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IPR003797; DegV.
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TIGRFAMs; TIGR00762; degV; 1.
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; Mismatches 0;
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Q927e0 listeria in
Q9zgzz yersinia pe
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Q8y3x8 listeria mo
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Q8zq21 salmonella
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Q9z3s8 pseudomonas
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ALIGNMENTS

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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 4.8 kDa protein (Fragment).
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                       MEDLINE=21036610; PubMed=11163452; Spielmann T., Beck H.P.; Spielmann T., Beck H.P.; "Analysis of stage-specific transcription in Plasmodium falciparum reveals a set of genes exclusively transcribed in ring stage parasites."; Mol. Biochem. Parasitol. 111:453-458(2000). EMBL; AJ290921; CAB92930.1; -.
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                Hypothetical protein.
                                                                                                                                                                                                                                                                                                              STRAIN=3D7
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                                                                                     23 SYDA 26
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Similarity 100.0%;
4; Conservative 0;
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                                                                                                                                                                                    AA; 4758 MW;
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                                                                                                                                    Score 21; DB 5; 1
Pred. No. 2.7e+02;
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Q9X374 PRELIMINARY;
Q9X374;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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Q12081;
01-NOV-1996
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EMBL; M15168; AAA66931.1; --
EMBL; M15167; AAA66930.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87120291; PubMed=3027892; Parikh V.S., Morgan M.M., Scott R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003583; BAB72673.1;
EMBL; AP003583; BAB72673.1;
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Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Nostoc. NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parikh V.S., Morgan M.M., Scott R., Clements L.S., Butow R.A., The mitochondrial genotype can influence nuclear gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMID-2-MICRON;
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AA;
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6029 MW; 42F9CC5A554CFF40 CRC64;
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Q9RIC5;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2002
Q9MC41
                                                                                                                                                                                                     STRAIN-CO-92 / BIOVAR ORIENTALIS; | MEDLINE-21470413; PubMed-11586360; | MEDLINE-21470413; PubMed-11586360; | Parkhill J. Wren B.W. Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton.J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague. BMBT. at117211. OMB62378 1.
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                     EMBL; AL117211; CAB62375.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical YPMT1.68A.
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Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter I
Martinez Y., Ricke D., Svensson R., Jackson P.J.;
"Sequence and organization of px01, the large Bacillus anthracis
plasmid harboring the anthrax toxin| genes.";
J. Bacteriol. 181:5509-6515(1999). |
EMBL; AF065404; AAD32409.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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Bacillus anthracis.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
1 protein YPMT1.68A.
PRELIMINARY;
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01-OCT-2000
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Pfam; PF00817;
Plasmid. 78
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SEQUENCE 78 AJ
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Q9Z3S8;
Q1-MAY-1999
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                                                                                                                MEDLINE=97080503; pubMed=8921848;
Sundin G.W., Kidambi S.P., Ullrich M., Bender C.,
"Resistance to ultraviolet light in Pseudomonas;
functional analysis of the plasmid-encoded rulab
Gene 17:77-81(1996).
EMBL; AJZ24510; CAB37318.1; -.
InterPro; IPR001126; UMUC_like.
                                                                                                                                                                                                                                                                                                                                                                                                                   "Replication regions from plan plasmids are similar to ColE2-Microbiology 145:325-334(1999)
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Plasmid pPT23A.
Bacteria; Proteobacte
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"Sequence of the Genome of the Temperate,
Pseudomonas aeruginosa Bacteriophage D3.";
J. Bacteriol. 182:6066-6074(2000).
EMBL; AF165214; AAF80767.1; -.
SEQUENCE 77 AA; 8266 MW; 39DAE91077F72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=31535;
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Viruses; dsDNA viruses,
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Maddeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell I
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vasquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Comparative genomics of Listeria species."; Science 294.849-852(2001), EMBL; AL596173; CAC98075.1; -. Listilist; LIN02849; -. Hypothetical protein; Complete proteome. SEQUENCE 80 AA; 9908 MW; B625A9DF7CF7CAD6 CRC64;
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Listeriaceae; Listeria
NCBI_TaxID=1642;
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  MEDLINE=99043898; PubMed=9826348; Lindler L.E., Plano G.V., Burland
                                          STRAIN-KIM10+;
                                                              SEQUENCE FROM N.A.
                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                       Yersinia pestis.
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RESULT

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                                                                                                                                                                                                                                                                                                                       Q8Y3X8
Q8Y3X8;
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2002
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T. Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussur Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
                                                                                                        STRAIN-EGD-E / SEROVAR 1/2A;
MEDLINE-21537279; PubMed-11679669;
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                   Bacteria; Firmicutes; I
Listeriaceae; Listeria
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01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                   Hypothetical LMO2701.
                                                                                                                                                                                                  NCBI_TaxID=1639;
                                                                                                                                                                                                                                                         Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
SEQUENCE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001126; UN Pfam; PF00817; IMS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Plant Pathol. EMBL; AJ251482; CA
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01-OCT-2000 (TrEMBLrel. 15, L
01-JUN-2002 (TrEMBLrel. 21, L
Hypothetical 9.3 kDa protein.
Pseudomonas syringae (pv. pis
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Hypothetical protein;
CECHTENCE 81 AA; 89/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-RACE 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arnold D.L., Jackson R.W., "Evidence for the mobility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9K510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete DNA sequence and detailed KIM5 plasmid encoding murine toxin a Infect Immun. 66:5731-5742(1998). EMBL; AF074611; AAC82735.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
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4; Conser
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al protein lmo2701.
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ilarity 100.0%;
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gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                                                                                                                                              Created)
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             races
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aces of Pseudomonas syringae pv.
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RA Borkova D., Bocchiam R.R., Cadieu E., Center A., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Daven R., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C., FRA Horris D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., FRA Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Vence R., Wang A.H., Wang X., Vence R., Vence R., Vence R., Vence R., Van S., Van Q.A.,
                RESULT

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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Butler H., Caddeu E., Center A., Chandra I.,
Charry J. M. Cauleu S., Butler H., Caddeu E., Center A., Chandra I.,
Charlev S., Butler H., Caddeu E., Center A., Chandra I.,
Charlev S., Butler H., Caddeu E., Center A., Chandra I.,
Charlev S., Butler H., Caddeu E., Center A., Chandra I.,
Charlev S., Butler H., Caddeu E., Center A., Chandra I.,
Charlev S., Butler H., Caddeu E., Center A., Chandra I.,
Charlev S., Chandra C., Charlev S., Chandra I.,
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01-MAY-2000
01-MAY-2000
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG16713.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Brachveera; Musc
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EMBL: AL591984; CAD00914.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gautier L., Goebel W., Gomez-Lopez N., H
Jones L.-M., Kaerst U., Kreft J., Kuhn M
Madueno E., Maitournam A., Mata Vicente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
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Neoptera; Endopterygota; Dip
a; Drosophilidae; Drosophila.
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C94155A9DB68BAFB CRC64;
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Kuhn M., Kunst F., Kurapi
Toente J., Ng E., Nedjari
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edjari H.,
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RESULT 14
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HSSP; P02760; IBIK.
FlyBase; FBgn0031560; CG16713.
InterPro; IFR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 1.
PFANTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
SMART; SM00131; KU; 1.
O8X8N9 PRELIMINARY;
O8X8N9;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
Orf, hypothetical protein
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Q8ZQ21;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE008750; AAL20091.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 84 AA; 9717 MW; 078AF3C835A3342F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
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PROSITE; PS50279; BPTI_KUNITZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
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u S., Zhu
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X., Smith H.O.,
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01-AUG-1998
01-MAR-2002
SEQUENCE FROM N.A.

Reeves C.D., Soliday C.L.;

"Analysis of a 27 kb region of Streptomyces roseofulvus containing genes for fremolicin biosynthesis.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AFOS8302; AACI8105.1; -.

InterPro: IPR00380; Ppantne_attach.

Pfam; PF00550; pp-binding; 1.

PROSITE; PS50075; ACP_DOMAIN; 1.
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MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001);

EMBL; AE005316; AAG55806.1; -.

EMBL; AP02555; BAB34861.1; -.
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                                                                                                                                                                                                                                                                                                                                                                         Streptomyces genes probably encoding antibiotic frenolicin."; Gene 142:31-39(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-94237486; PubMed-8181754;
Bibb M.J., Sherman D.H., Omura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales;
NCBI_TaxID=33902;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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MEDLINE=21074935; PubMed=11206551;
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Escherichia coli 0157:H7.
Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bibb M.J., Sherman D.H., Omura S., Hopwood D.A.; "Cloning, sequencing and deduced functions of a cl
Streptomyces genes probably encoding biosynthesis
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STRAIN=0157:H7 / E
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                                                                            STRAIN-FRIEDLIN;
Murphy T
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"Complete genome sequence of a multiple enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
EMBL; AL627269; CAD08285.1; -.
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Hypothetical
NON_TER
SEQUENCE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkhout R.J.M., Bouwes Bavinck J.N., ter Sche Persistence of Human Papillomavirus DNA in Be Skin Lesions from Renal Transplant Recipients J. Clin. Microbiol. 38:2087-2096(2000). EMBL; AR054881; AA012747.1; InterPro; ITR002210; PV_capsid_L1. Ffam; PF00500; late_protein_L1; 1. Prodom; PD000544; PV_capsid_L1; 1.
                                              Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; BC010220; AAH10220.1; -. InterPro; IPR002005; Rab_GDI_REP. | Pfam; PF00996; GDI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                     Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                      Mus musculus (Mouse)
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NCBI_TaxID=10566;
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                                                                                                                             Strausberg
                                                                                                                                                SEQUENCE FROM
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STRAIN-HPVX24
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10620
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 74DBAE69BBAB5FA6
                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
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Murinae; Mus
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                       C STRAIN-GMI1000;

X MEDLINE-21681879; PubMed-11823852;

A Salanoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot S.,

A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

A Arlat M., Billault A., Brottier P., Camus J.C., Cunnac S., Demange l

A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange l

A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

A Weissenbach J., Boucher C.A.;

A Weissenbach J., Boucher C.A.;

T "Genome sequence of the plant pathogen Ralstonia solanacearum."

T "Genome sequence of the plant pathogen Ralstonia solanacearum."

IN ALMIC S. CAD14830.1;

NA LISTAIN ALGAGOGE; CAD14830.1;

R EMBL; ALGAGOGE; CAD14830.1;

R EMBL; ALGAGOGE; CAD14830.1;

R SEQUENCE 96 AA; 10601 MW; 960D8A89DB418D60 CRC64;
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085877;
01-NOV-1998
01-NOV-1998
01-DEC-2001
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sphingomonas aromaticivorans
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                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria: Proteobacteria; beta subdivision; Ralstonia
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57 SYDA 60
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
1 10.5 kDa protein.
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Pred. No.
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Pred. No. 6.6e+02;
Nismatches 0;
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Schiex T.,
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014371;
01-JAN-1998
01-JAN-1998
01-DEC-2001
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Jang Y.-J., YOO H.-S.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ
EMBL; U97365; AAB63857.1;
InterPro; IPR000517; Ribosomal_L30.
InterPro; IPR000517; Ribosomal_L30; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
60S ribosomal protein L7B (Fragment).
Schizosaccharomyces pombe (Fission yeast).
                                                                   STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome clone:B1142C05.";
                                                                                                                                                                                                                  Q8SOG9;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                 Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003410; BAB89131.1; -
                                                                                                                                           Oryza sativa (japonica cultivar group).
Eukaryota; Viridiplantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                     B1142C05.31 protein.
B1142C05.31.
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                                                                                                                SEQUENCE FROM N.A.
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thes 0;
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O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 11.4 kDa protein.
ORF680.
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01-JUN-2002
01-JUN-2002
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STRAIN-ATCC 25586;

MEDLINE-21886394; PubMed-11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis /
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium fusobacterium
nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).

EMBL; AE010519; AAL94251.1; ".
                                                                                                   Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sensen C.W., Gaasterland T., Saffer J.D., Fredrickson J. "Complete sequence of a 184 kb catabolic plasmid from Sparomaticivorans strain F199.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF079317; AAD03931.1;
                                                                                                                                                                                                                        Bacteria; Proteobacteria; Novosphingobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 10
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63 SYDA 66
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                                                                               l protein; Plasmid.
103 AA; 11444 MW;
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ilarity 100.0%;
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01-JUN-2001
01-JUN-2001
01-DEC-2001
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01-MAR-2001
01-MAR-2001
                                                                                        Complete
SEQUENCE
                                                                                                                               MEDLINE=20504483; PubMed=11016950; Mg W.V., Kennedy S.P., Mahairas G.G., Berguist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S.; Thorsson V., Sbrogna J., Shukla H.D., Lasky S.R., Baliga N.S.; Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Rieby M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferretti J.J., McShan W.M., Ajdic D.J., Savic G. Frimeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Qian Y., Jia H.G., Najar F.Z., Ren IQ., Zhu H., Song L., Whi Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halobacterium sp. (strain NRC-1). |
Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
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STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINE=21192684; PubMed=11296296;
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NCBI_TaxID=1314;
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                                                DB 17;
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S., Lai H.S., Lir
, Song L., White
                                                                                           CRC64;
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Q8W5F8;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Q942U5;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
Vanaken S.E., Utterback T.R., Feldhlyum T.V., Kalb E., Quackenbus
Salzberg S.L., White O., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBb0008A05 genomic sequence."
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B., Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Utterback T.T., Feldblyum T.V., Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M., "Oryza sativa chromosome 10 BAC OSJNBa0073L20 genomic sequence."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC091749; AAJ31098.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice), and Oryza sativa (Japonica cultivar-group). Oryza sativa (Japonica cultivar-group). Eukaryota; Viridiplantae; Streptophyta; Er Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T
                                                                                                                              P0506E04.27
P0506E04.27.
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                                                                       Spermatophyta;
Ehrhartoideae;
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                                                                                                                Oryza sativa (Rice).
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67 SYDA 70
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                                                                     Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; yta; Magnoliophyta; Liliopsida; Poales; Poaceae; eae; Oryzeae; Oryza.
                                                                                                                                          protein.
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(TTEMBLrel. 20, Last sequence update)
(TTEMBLrel. 21, Last anotation update)
[11.2 kDa protein (Putative rapid alkalinization factor
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  Yamamoto K.;
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Last sequence update)
Last annotation update)
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Pred. No. 7.9e+02;
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Q9XCB3;
01-NOV-1999
01-NOV-1999
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EMBL; AP003272; BAB67949.1; -.
InterPro: IPR002086; Aldehyde_dehydr.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1
SEQUENCE 111 AA; 11334 MW; 74AB4291D5334A2A
STRAIN-ITI 376;
Thorolfsdottir E.T.T., Backman V.M.,
Thorolfsdottir S.H., Palsdottir A
Thorbjarnardottir S.H., Eggertsson G.;
Kristjansdottir S., Eggertsson G.;
                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Putative O-methyltransferase (Fragment)
                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20428552; PubMed=10970881; Mitrovich Q.M., Anderson P.; "Unproductively spliced ribosomal protein mRNA surveillance in C. elegans."; Genes Dev. 14:2173-2184(2000).
                                                                  Rhodothermus marinus Bacteria; CFB group; NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE L1P EMBL; AF247854; AAF77035.1; -. InterPro; IPR002143; R1bosomal_L1.
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Eukaryota; Metazoa; Nem
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-UN-2002 (TrEMBLrel. 21, Last annotation
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                                             SEQUENCE FROM N.A.
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NCBI_TaxID=31234;
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                                                                              Rhodothermus
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Q95WK3;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2002
                                                                                           Bacteria; Thermus/Deinococcus Deinococcaceae; Deinococcus.
                                                                                                                                          Plasmid MP1
                        SEQUENCE FROM N.A.
                                                      NCBI_TaxID=1299;
[1]
                                                                                                                                                              Deinococcus radiodurans.
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EMBL, AB317810; AAL18429.1; -. Interpro; IPR001182; GEPD.

Pfam; PF00479; GEPD; 1.
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Eukaryota; Metazoa; Arthropoda;
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF145250; AAD37972.1; -
InterPro; IPR00293; Methyltransf_3.
Pfam; PF01596; Methyltransf_3; 1.
Methyltransferase; Transferase.
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113 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
hosphate dehydrogenase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0
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13423 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arthropoda; Tracheata; Hexapoda; Ins.
Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 5; Pred. No. 8.2e+02; Pred. No. 8.2e+02;
                                                                                                            group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Pred. No.
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                                                                                                            Deinococci;
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s 0;
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                                                                                                               Deinococcales;
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RESULT 35
Q92J3
ID Q92J3
AC Q92J3
AC Q92J3
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OS Ricke
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Q8RSN6
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Best Local 9
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Best Local
                                              Q92J33
Q92J33;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
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Q8RSN6;
O1-JUN-2002 (TrEM
O1-JUN-2002 (TrEM
O1-JUN-2002 (TrEM
UPF54.8 protein.
                Rickettsia
                                     Hypothetical protein
                                                                                                                                                                                                                                                                    "The IncP beta plasmid pB4 encodes a tripartite antibiotic system of the RND-MFP-OEP type conferring erythromycin and roxithromycin resistance in Pseudomonas sp. B13."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AJ431260; CAD24324.1; -...
    Bacteria;
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          uncultured bacterium.
Plasmid pB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20036896; PubMed=10567266; | Milte O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Wolfat K.S., Qin H., Jung L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Wakarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                 Plasmid
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Bacteria; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001826; AAF12594.1; .
TIGR; DRB0072; .
TIGR; DRB0072; .
TIRP000733; Flav_monooxygnse.
InterPro; IPR000733; Flav_monoxygnse.
InterPro; IPR000742; Rng_mnoxygnse.
PfinterPro; IPR003042; Rng_moxygense.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=77133;
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SEQUENCE 113
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                                                                                                                                                         93 SYDA
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4; Conservative
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  Proteobacteria;
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(TrEMBLrel.)
                                                (TrembLrel. 19, Created)
(TrembLrel. 19, Last seq
(TrembLrel. 19, Last ann
                                                                                             PRELIMINARY;
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AA; 12561 MW; 9DE2C58D930A6D73 CRC64;
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                                     RC0236
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Last annotation update)
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Pred. No. 8
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Pred. No. 8
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subdivision;
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hes 0;
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s 0;
 Rickettsiales
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RESULT 37
Q92US4
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Q991X7
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Best Local S
Matches 4
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Best Local
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Q991X7;
Q1-JUN-2001
Q1-JUN-2001
Q1-DEC-2001
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Raoult D.;
                                                                                                                            Putative regulatory protein, arsk family. RB1016 OR SMB21576.
Rhizobium meliloti (Sinorhizobium meliloti). Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mechanisms of evolution in Rickettsia conorii a Science 293:2093-2098(2001).
EMBL; AE008591; AAL02774.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 115 AA; 13298 MW; C419CB796D5BD8A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      natural environments.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ EMBL; AF340050; AAK28563.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stokes H.W., Nield B.S., Gillings M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uncultured organism.
unclassified; enviro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat.
Hypothetical 12.8 kDa protein.
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STRAIN-MALISH 7;
MEDLINE-21442074; PubMed-11557893;
STRAIN=1021;
MEDLINE=21396508; PubMed=11481431;
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NCBI_TaxID=781;
                                             SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=382;
                                                                                                        Rhizobiaceae; Sinorhizobium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Novel and diverse integron-like
                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  environmental samples
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Cossart P., Weissenbach
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Pred. No. 8.4
); Mismatches
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Pred. No. 8.3e+02;
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                                                                                                                            subdivision; Rhizobiaceae group;
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Best Local (
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Q9XVLO;
01-NOV-1999 (TrembLrel. I
01-NOV-1999 (TrembLrel. I
01-DEC-2001 (TrembLrel. I
                                                                P73361;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Hypothetical protein slr1210.
                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                  EMBL; Z81101;
                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001845; HTH_ArsR. Pfam; PF01022; HTH_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti."; proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL; AL603645; CAC49416.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finan T.M., Weldner S., Wong K., Buhrmester J., Chain Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie Golding B., Puehler A.;
                                                                                                                           P73361
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                         none;
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12870 MW; 466B316B40ED46C1 CRC64;
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SEQUENCE FROM N.A. MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Ta

Tanaka

Α.,

Asamizu

Nakamura

Synechocystis sp. (strain Bacteria; Cyanobacteria; Cyanobacteria; CBI_TaxID=1148;

(strain

PCC 6803)

Chroococcales;

Synechocystis

update)

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Best Local
Q9NBK3

Q9NBK3;
Q9NBK3;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-MAR-2001 (TrEMBLrel. 17, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Hypothetical protein SAV0273.
SAV0273 OR SA0262.
Staphyloro---
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Q99WV3;
Q1-JUN-2001
Q1-JUN-2001
Q1-MAR-2002
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EMBL; AP003358; BAB56435.1; -.
EMBL; AP003130; BAB41486.1; --
HYpothetical protein; Complete
SEQUENCE 130 AA; 15765 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-S.aureus (strain Mu50), an MEDLINE-21311952; PubMed-11418146;
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NCBI_TaxID=158878,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimpo S., Tabata S.;
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SEQUENCE 12
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i T., Matsuno
S., Takeuchi C
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129 AA; 14936 MW;
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Matsuno A., Muraki A., Nakazaki N., Naruo K.
Akeuchi C., Wada T., Watanabe A., Yamada M.,
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15765 MW;
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Pred. No. 9.5e+02;
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A3F692D13BD7B764 CRC64;
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aruo K., Okumura
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Q8X858;
Q1-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002 (TrEMBLrel. 2001-MAR-2002)
                                                           STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

EMBL; ARO05257; AAG55129.1; -...

EMBL; ARO05253; BAB34258.1; ALT_INIT.
                                                                                                                                                                                                                                                                       Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                       Nature
[2]
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SEQUENCE FROM N.A.

MEDLINE-20428552; PubMed-10970881; |

Mitrovich Q.M., Anderson P.;

"Unproductively spliced ribosomal protein mRNAs

"Unproductively spliced ribosomal protein mRNAs

"Unproductively spliced ribosomal protein mRNAs

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Escherichia coli O157:H7.
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NCBI_TaxID=83334;
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Genes Dev. 14:2173-2184(2000).
-!-SIMILARITY: BELONGS TO THE LIP
EMBL; AF247848; AAF77029.1; -.
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Rhabditidae;
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TE; PS01199;
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                                                      proteome.
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132 AA;
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e; Peloderinae;
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ilarity 100.0%;
Conservative (
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                                          ΑA;
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132
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Last annotation update)
prophage CP-933K (Putative
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Score |21;
Pred. No.
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Pred. No. 9.6
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      subdivision;
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DB 16;
9.6e+02;
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s 0;
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                                                                                                                                              N., Yasunaga
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            132;
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Tobe T.,
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RESULT 44
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ID 039HH
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AC Q97HH
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                                                                  SEQUENCE FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

MEDLINE-21359325; PubMed-11466286;

Noelling J. Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

EMBL; AB007699; ANX79882 1;

InterPro; IPR000424; SSB_protein.

Pfam; PF00436; SSB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium acetobutylicum.

Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  097HT8.
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Investigating biology.";
Science 282:2012-2018(1998).
EMBL; 282076; CAB04936.1; -.
SEQUENCE 133 AA; 15587 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phage related SSB-like CAC1919.
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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                                               TIGRFAMS; TIGRO0621; ssb;
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96 SYDA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 SYDA 90
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14980 MW;
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100.0%; Pred. No. 9.7e+0;
Live 0; Mismatches
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FOFCOOCEBF938EDB CRC64;
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RESULT 45
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

MEDLINE-21359325; PubMed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183,4823-4838(2001).

EMBL; AE007774; AAK80711.1;

Complete proteome.

132 AA. 14776 MM. AE07DA2063381FIC CRC64.
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O97FH2; O1-OCT-2001 (TrEMBLrel. 18, Created)
O1-OCT-2001 (TrEMBLrel. 18, Last sequence up
O1-OCT-2001 (TrEMBLrel. 18, Last annotation
                                                                                                                                                                 SEQUENCE
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9.7e+02;
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9.7e+02;
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Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
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19.150 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                 Length
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     AAR72768
AAW70154
AAW46010
AAY96208
AAY83850
AAE05612
AAW13438
AAB07398
AAB07398
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Mammalian ribonucl
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Peptide #1 based
Arabidopsis AHAS s
Ribonucleotide red
N-terminal CT27 pe
Brain homing pepti
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18	21	19	16	18	23	22	14	20	21	14									21	20	19	21	21	21	21	21	22	19	16	22	21	23	23	22
AAW10869	AAY95418	AAW31683	AAR71050	AAW10854	AAU88904	ABB51179	AAR33356	AAY36691	AAY91397	AAR36604	AAY95420	AAR93618	AAM97480	AAM97105	AAY93098	AAY92950	AAB84497	AAG79149	AAB20756	AAW74421	AAW69624	AAY93093	AAY93009	AAY93008	AAY93007	AAY92947	AAG86956	AAW61058	AAR72570	AAB99639	AAY93097	AAU10715	ABG67883	AAE11804
MAb anti-HBsAg bin	Anti-angiogenic D3	um perf	Draculin peptide #	MAb anti-HBsAg bin	Insulin/insulin-li	creted pr	of.	Fragment of human	rg T	N-terminus of 37 k	Anti-angiogenic D3	cincipal	Human peptide #755	Human peptide #380		Transforming growt	Amino acid sequenc	Amino acid sequenc	a-Mid-5 libr	agonist						Transforming growt	s cer		llium	Q.		homin	ADPI trypt	Phage peptide #12

ALIGNMENTS

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RESULT 1
AAR72768
Plasmodium falciparum; mammalian; ribonucleotide reductase; R2 subunit; C-terminal region; inhibitor; antimalarial therapy; Pf RR; parasite.
                                                                                                                                     Key
Modified-site
                                                                                                                                                             Synthetic
       WPI; 1995-161730/21
                       Cooperman BS, Fisher AL,
                                       (UYPE-) UNIV PENNSYLVANIA.
                                                         14-OCT-1993;
                                                                         07-OCT-1994;
                                                                                            20-APR-1995.
                                                                                                            WO9510526-A1
                                                                                                                                                                                                         Mammalian ribonucleotide reductase inhibitory peptide.
                                                                                                                                                                                                                          02-FEB-1996
                                                                                                                                                                                                                                             AAR72768;
                                                                                                                                                                                                                                                            AAR72768 standard; Protein; 7
                                                                                                                                                                                                                           (first entry)
                                                          93US-0136743
                                                                          94WO-US11416
                                                                                                                                      Location/Qualifiers
                                                                                                                             /note= "opt. acylated"
                       Rubin H,
                        Salem
                        J,
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AAU68419

Breast cance

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В
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
Sequences AAW70114, AAW70142-W70154 are N-terminal amino acid sequences of peptides generated by chymotrypsin/trypsin digestion of the 45 kDa Mp7 32 91ycoprotein. These sequences were obtained by purifying the 45 kDa protein, digesting it with chymotrypsin/trypsin, and then separating the products by reversed-phase HPLC on a column. All of the peptides were
                                                                                                                  Early detection of mycobacterial infection - fluid sample from a subject for the presence with Mycobacterium tuberculosis antigens
                                                                                              Example
                                                                                                                                                                                  WPI; 1998-387787/33.
                                                                                                                                                                                                                                         (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                      29-DEC-1997;
                                                                                                                                                                                                                                                                                                                                  09-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                               W09829132-A1
                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                       prokaryote;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycopeptide; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW70154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW70154 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum ribonucleotide reductase (Pf RR) sub-units -also DNA and peptide(s) derived from sub-unit R2 C-terminus useful in antimalarial compsns as specific inhibitors of Pf RR activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                            Page
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                                                                                                                                                                                                                                                                                                                                                                                           tuberculosis.
                                                                                                                                                                                                                                                                       96US-0034003
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                                                                                         72; 170pp;
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100.0%; f
tive 0;
                                                                                                                                                                                                             Zolla-Pazner
                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Spectrometry;
                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin; reversed-phase HPLC; FAB-MS; Spectrometry; Edman degradation; mycob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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Pred. No. 7
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.8e+05;
s 0;
                                                                                                                                     ьy
                                                                                                                                                                                                                                                                                                                                                                                                                              degradation; mycobacteria;
                                                                                                                                  testing a biological antibodies reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7;
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                                                                                  Peptides AAW45983-W456025 are based on portions of somatostatin, somatostatin receptors (SSTR) and insulin-like growth factor binding proteins (IGFBP). They are capable of increasing weight gain, birth weight, growth rates, milk production, levels of circulating insulin, IGF-I and IGF-III, fibre production and muscle weight. They may be used to modulate carbohydrate metabolism and in treatment of diabetes. The oil carrier may be used for delivery of the peptides.
                                                                   Sequence
                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                New non-naturally occurring peptide(s) - which are based of somatostatin, somatostatin receptors and insulin-like
                                                                                                                                                                                                                                                      WPI; 1998-018427/02
                                                                                                                                                                                                                                                                                                (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subjected to both Fast Atom Bombardment-Mass Spectrometry (FAB-MS), automated Edman degradation to determine their molecular weight and N-terminal amino acid sequence, respectively. The discovery of the complete primary structure of MPT 32 glycoprotein enables further we to be performed and the possibility of it being used as an antigen f
                                                                                                                                                                                                         factor binding
                                                                                                                                                                                                                                                                                                                        22-MAY-1996;
                                                                                                                                                                                                                                                                                                                                              22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                          W09744352-A1
                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  somatostatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW46010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW46010 standard; peptide;
                      Local Similarity
nes 4; Conser
1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                    7
                      Conservative
                                                                                                                                                                                  Page 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               based
                                                                  AA;
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receptor;
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                                                                                                                                                                                                                                                                          Westbrook SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSTR 4 (residues 282-290).
                      0;
                    Score 18; DE
Pred. No. 7.8
0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                growth factor.
                              DB 19;
7.8e+05;
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                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    somatostatin;
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AAY96208
ID AAY96208
ID AAY9
XX AAY9
XX AFAB
XX Herb
KW Herb
KW Erfia
KW Dyri
KW Dyri
KW Dyri
KW Dyri
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KW Cria
KW Dyri
KW ACet
KW Herb
KW WO20
XX AFAB

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                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis acetohydroxy-acid synthase (AHAS) small subunit is needed CC for branched-chain amino acid synthesis and so is essential for life. CC AHAS is also known as acetolactate synthase. Inhibition of this enzyme CC in plants would lead to plant death and therefore inhibitors would be potential herbicides. Certain herbicides are known to inhibit AHASs: CC imidazolinones, sulfonylureas, triazolpyrimidine sulfonamides. CC pyrimidyl-cvy-benzoic acids, sulfamoylureas and sulfonylaraboxamides. CC Mutant AHAS may be resistant to these herbicides and may be used to CC create herbicide resistant transgenic plants e.g. dicot and monocot crop plants. A thrombin cleavage site was incorporated into an AHAS small companies. A thrombin cleavage site was incorporated into an AHAS small subunit gene fragments were cloned into CC plasmid expression vectors, and were expressed as glutathione CC transferase was then cleaved via the thrombin cleavage site. Cleavage transferase was then cleaved via the thrombin cleavage site. Cleavage core details the CC are maintained on the AHAS protein. The present sequence details the CC are maintained on the AHAS protein. The present sequence details the CC are maintained on the AHAS protein and serine residues of the cleavage site CC are maintained on the AHAS protein. The present sequence details the CC and filarion due to cleavage site and serine residues of the cleavage site CC are maintained on the AHAS protein. The present sequence details the CC and filarion due to cleavage site site and serine residues of the cleavage site composition of the cleavage site composition of the coleavage site coleavag
                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetolactate synthase; imidazolinone; sulfonylurea;
triazolopyrimidine sulfonamide; sulfamoylurea; enzyme;
pyrimidyl-oxy-benzoic acid; sulfonylcarboxamide; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding eukaryotic acetohydroxy-acid synthetase small subunit protein for producing transgenic herbicide resistant protein for producing transgenic herbicide resistant small identifying mutations affecting enzymatic activity of the
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kakefuda G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200026390-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herbicide-resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis AHAS small subunit F2 gene fragment N-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY96208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96208 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                   modification due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                branched-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-2000
                                                                                                                                                                               Local Similarity
N
                                                                    1 SLDA 4
SLDA
                                                                                                                                             4,
                                                                                                                                                                                                                                                                                              7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 25;
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Costello C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0106239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US25452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                      ç
                                                                                                                                                                                                                                                                                                                                                                   cleavage.
                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acetohydroxy-acid synthase; AHAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthesis
                                                                                                                                             0;
                                                                                                                                     Score 18; DB 21,
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Σ
                                                                                                                                                                                                              Length
                                                                                                                                             Indels
                                                                                                                                         0;
                                                                                                                                         Gaps
                                                                                                                                         0;
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RESULT 5

Mycobacterial disease; infection; 88-kDa protein; tuberculosis; human immunodeficiency virus; HIV; CT27 glycopeptide; serodiagno

peptide obtained by proteolysis of Mt 45 kDa antigen

0

N-terminal CT27

(first entry)

AAE05612;

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RESULT 6
AAE05612
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ID AAY8
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                                                                                                                                                                                                                                      EXXEXEX EX EX X B
                                                                                                                                                                     Q
                                                                                                                                                                                         Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                       The invention relates to a composition comprising a peptide inhibitor of ribonucleotide reductase. Peptides AN/83839-Y83864 represent examples of the inhibitor peptides used in the composition. The peptides are synthesised based on the sequences of known mammalian, bacterial and viral ribonucleotide reductases. The compositions are used in the treatment of disorders associated with DNA replication, such as tumour growth and metastasis and infectious disease, such as those caused by viruses, bacteria, fungi and parasites.
                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; antibacterial; virucide; antifungal; parasiticide; virus; antimetastatic; ribonucleotide reductase; peptide inhibitor; bacteriu DNA replication; tumour growth; metastasis; fungus; parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY83850
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-223191/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-AUG-1996;
28-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6030942-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribonucleotide reductase inhibitor peptide #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY83850 standard; peptide;
                                                                                           AAE05612 standard; peptide; 7
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cooperman BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-FEB-2000
                                                                                                                                                              1 SLDA 4
                                                                                                                                                   N
                                                                                                                                                   SLDA
                                                                                                                                                                                            4.
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                      7
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nair S, Fisher A,
                                                                                                                                                                                                                                      Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0025146.
97US-0919748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0040216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "acetylated N-terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                      92pp; English.
                                                                                                                                                                                            0
                                                                                                                                                                                                     Score 18; DB 21;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Laub P, S
Smith AB;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasho
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ś
                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sprengeler
                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterium;
                                                                                                                                                                                            Gaps
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RESULT 7
AAW13438
ID AAW1
XX
AC AAW1
AC AAW1
XX
DT 15-J
XX
DF Brai
XX
Brai
XX
Brai
XX
Synt
XX
W097
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                                                                                                                                                                                                                                                                                                                                            γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC mycobacterial disease or infection comprises assaying a biological fluid CC sample for the presence of early antibodies pecific for an 88 kDa CC Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of CC an 88 kDa M. tuberculosis protein antigen or immune complexes consisting of CC an 88 kDa M. tuberculosis protein antigen complexed with an antibody CC detection of mycobacterial disease, particularly tuberculosis; in CC individuals at heightened risk of developing tuberculosis (TB). This CC individuals include human immunodeficiency virus (HIV)-infected subjects or other immunocompromised individuals. The method is a rapid and CC inexpensive screening procedure for detecting mycobacterial disease. CC or other immunocompromised individuals. The method is a rapid and CC inexpensive screening procedure for detecting mycobacterial disease. CC glycopeptide. The N-terminal amino acid sequence of CT27 CC glycopeptide. The N-terminal amino acid sequence of CT27 CC glycopeptide. The N-terminal applide is identified by fast atom CC sequence analysis of peptides generated by proteolysis of CC Mt 45 kDa/MPT 32 glycoprotein with chymotrypsin/trypsin. The Mt 45 kDa/MPT 32 early antigen is used in the serodiagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                 W09710507-A1
                                                                               Brain homing peptide; in vivo panning; screening; phage display;
                                                                                                                           Brain homing
                                                Synthetic
                                                                                                                                                                                                AAW13438;
                                                                                                                                                                                                                          AAW13438 standard; Peptide; 8
                                                                                                                                                              15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Column 46; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen-antibody complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a mycobacterial disease (tuberculosis) in individuals comprise assaying a biological sample for the presence of anti-Mycobacterium tuberculosis antibodies or M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laal S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fast atom bombardment-mass spectrometry; FAB-MS; proteolysis;
45 kDa glycoprotein; MPT 32; chymotrypsin; trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNY-) UNIV NEW YORK MEDICAL CENT. (COLS ) UNIV COLORADO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                              4 SLDA
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                               1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to a method for early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-424324/45
                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zolla-Pazner
                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                           peptide
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            ĀĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0034003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0001984
                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Belisle
                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 22;
Pred. No. 7.8e+05;
Mismatches 0;
                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection of active
                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 8
AAB07398
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                   11-SEP-1995;
10-MAR-1997;
          (BURN-) BURNHAM INST
                                                                                                                                                                                                                   Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.
                                                                        23-JUN-1997;
                                                                                                                         US6068829-A
                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                  Mus sp
                                                                                                                                                                                                                                                   Brain homing
                                                                                                                                                                                                                                                                            17-OCT-2000
                                                                                                                                                                                                                                                                                                     AAB07398
                                                                                                                                                                                                                                                                                                                          AAB07398 standard; peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identified in vivo, as compared to prior art in vitro screening methods, which require further examination to see if they maintain specificity in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This synthetic peptide is an example of a brain-homing peptide that was identified using a claimed method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method typically involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, anglogenic vascular tissue or timour tissue. The isolated peptides (see AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins olabels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed): The peptides can be directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Obtaining compound that homes to selected organ or tissue - by vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-202359/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LJOL-) LA JOLLA CANCER RES FOUND .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-1995;
11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                        SLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 18; DB 18; llarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                  peptide # 12.
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                 95US-0526710.
97US-0813273.
                                                                       97us-0862855
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruoslahti E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0526710
95US-0526708
                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US14600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75pp; English.
                                                                                                                                             "Can optionally form a
                                                                                                                                                                                                                                                                                                                          A
A
                                                                                                                                             cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                            peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 9
AAY56002
ID AAY5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence identified by using in vivo panning to screen a library corgan homing molecules. The present sequence can be used moiety to a the brain tissue, by linking the moiety to the moiety to a constant and moieties are drugs, toxing the model of section of potential moieties are drugs, toxing the model of section of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying and recovering organ homing molecules or peptides by in vivo panning comprises administering a library of diverse peptides linked to a tag which facilitates recovery of these peptides -
                                    sequence for isolating the corresponding gene. The protein is useful for the specific cleavage of complex sugar chains for the preparation, investigation and modification of these chains, especially in complex carbohydrates forming part of a glycoprotein molecule which undergoes
                                                                                                                                     Peptides AAY55994-Y56014 represent fragments of the Mucor hiemalis endo-beta-N-acety/glucosaminidase protein derived by cleavage with Lys-C protease and subsequent amino acid sequencing. The peptide sequences were then used to generate primers to isolate the coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                 Example 4; Page 22; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                               Polynucleotides encoding endo-beta-N-acetylglucosaminidase, useful for the specific cleavage of complex sugar chains -
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-062704/05
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kobayashi K,
Yoshida S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endo-beta-N-acetylglucosaminidase; enzyme; cleavage; sugar chain;
carbohydrate; glycoprotein; disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mucor hiemalis endo-beta-N-acetylglucosaminidase peptide p60-AP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY56002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY56002 standard; peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detectable label.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KIRI ) KIRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2000
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑĄ;
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                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BEER KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takeuchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0141717
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                  such
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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. 7.8e+05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide. This sequence van a library of potential can be used to direct a
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ζ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the present toxins or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumagai
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RESULT 10
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Matches
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                  or identifying the risk of a subject developing cancer (especially breast cancer), or monitoring the effect of therapy on a subject with cancer, comprising analysing a test sample using two-dimensional electrophoresis and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The methods disclosed are used for the diagnosis and prognosis of breast cancer, for determining the severity of breast cancer, and for identifying a subject at risk of developing breast cancer, and monitoring the effect of therapy administered to a subject. Antibodies raised against the binding domain of a BPI, the binding domain of a BPI, a nucleic acid encoding a BPI, or a nucleic acid that inhibits the function of a BPI can be incorporated into a pharmaceutical
                                                                                                      composition for treating or preventing breast cancer. The methods use sensitive and specific biomarkers provide early diagnosis of breast cancer, and the compositions are more potent, specific, and has a more rapid effect with fewer side effects that other prior art methods. The present sequence is a tryptic digest peptide from a BPI of the
                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying proteins for clinical screening, diagnosis and preast cancer, comprises detecting Breast Cancer-Associated Isoforms (BPIs) using two-dimensional electrophoresis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Breast cancer-associated protein isoform; brimmunogen; cytostatic; BPI; tryptic digest peptide.
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                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 51; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2000; 2000GB-0006695.
24-MAR-2000; 2000GB-0007265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Breast cancer-associated protein isoform, BPI-247 peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herath HMAC,
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                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OXFO-) OXFORD GLYCOSCIENCES UK LTD
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                                                                                                                                                                                                                                                                                                                                                              invention relates to diagnosing,
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llarity 100.0%;
Conservative (
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              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page MJ,
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Score 18; DB 22;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 21;
Pred. No. 7.8e+05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parekh RB,
                                                                                                                                                                                                                                                                                                                                                              determining the stage or severity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterfield MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast cancer;
                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 8;
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RESULT 11
AAE11804
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PN US629
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RESULT 12
ABG67883
ID ABG67
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AC ABG67
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DT 07-OC
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           Human ADPI tryptic digest peptide #592.
                                                                                                                                                                                 ABG67883 standard;
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11-SEP-1995;
10-MAR-1997;
                                                                             07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an enriched library fraction containing molecules that selectively home to a selected organ or tissue such as brain, kidney or tumour recovered by in vivo panning. The invention generally relates to the field of molecular medicine, drug delivery and to a method of invivo panning for identifying a molecule that homes to a specific organ. The molecules, e.g., peptides, peptidenmetics, proteins and fragments of proteins contained in an enriched library fraction may be administered to a subject as part of a pharmaceutical composition to rest disease or in diagnostic methods. The present sequence is a peptide from bacteriophage targetted to brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enriched library fraction comprising molecules recovered by in vivo panning that selectively home to a selected organ or tissue useful for treating disease or in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Column 17; 21pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enriched library fraction; brain; kidney; tumour; panning; diagnostic; molecular medicine; drug delivery; peptidomimetic; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6296832-B1
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||||
4 SLDA 7
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                                                                        (first entry)
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95US-0526710.
97US-0813273.
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                                                                                                                                                                                 Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DE Pred. No. 7.8
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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RESULT 13
AAU10715
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AC AAU10
XX 12-MA
CT 12-MA
XX U2-MA
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening, diagnosis or prognosis of Alzheimer's disease (AD) in a subject. The method comprises analysing a sample of brain tissue from a subject by 2D electrophoresis to generate a 2D array of 2C Alzheimer's disease-associated features (ADFs), whose relative abundance correlates with the presence, absence, stage or severity of 2D and comparing the abundance of each feature with the abundance of that chosen feature in brain tissue from persons free from AD. The 2C isoforms (ADPIs) detectable in brain tissue. The methods and 2C compositions of the invention are useful for the screening, diagnosis of AD in a subject, for determining the stage or severity of AD in a subject, for determining the stage or severity are in a subject, for identifying a subject at risk of developing AD, and for preventing AD, and for determining the stage or severity of treatment regime. An agent that modulates the activity of ADPI is cuseful in the manufacture of a medicament for the treatment or the prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI ax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                    Organ targeting; tissue targeting; cancer; tumour homing molecule
                        delivery of target molecule;
                                                                                                 Brain homing peptide #12 useful for delivery of target molecules.
                                                                                                                                                                          12-MAR-2002
                                                                                                                                                                                                                                                                              AAU10715 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to methods and compositions screening, diagnosis or prognosis of Alzheimer's disease (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening, diagnosis or prognosis of Alzheimer's disease in subject, comprises detecting Alzheimer's disease-associated features or Alzheimer's disease-associated protein isoforms in brain tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 65; 427pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-508575/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herath HMAC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200246767-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SLDA 4
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les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         بر
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                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rohlff C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                        brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                  homing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 7.8e+05;
ches 0;
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RESULT 14
AAY93097
ID AAY93
XX AAY93
XX AAY93
XX O8-NC
DT 08-NC
DT Trans
XX Hepat
KW Hepat
KW Compp
KW extra
XX Homo
XX Homo
XX Homo
XX Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the selected organ or tissue. The method comprises administering to the subject the library of diverse molecules, collecting a sample of the selected organ or tissue (e.g. brain or kidney), and recovering from the sample several molecules that home to the selected organ or tissue. The method is useful for identifying molecules, particularly useful for compression or descriptions. The identified molecule is useful for e.g. raising an compression of the selected organ. The identified molecule is useful for e.g. raising an compression of the selected organ. The identified molecule is useful for e.g. raising an compression of the selected organ. The identified molecule is useful for e.g. raising an compression of the selected organ. The identified molecule is useful for e.g. raising an compression of the presence of cancer that specific for a target molecule, targeting a desired moiety complex to the presence of cancer in a subject by linking an appropriate molecy to a tumour homing complex that specifically home to a selected organ and, therefore provides a significant advantage over previous methods, which require complex that specifically home to a selected organ and, therefore that a molecule identified using an in vitro screening method complex that specificity in the present brain homing peptides described in the present brain brain homing peptides described in th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
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11-SEP-1995;
10-MAR-1997;
                                                                                     Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; lextracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                 Transforming growth factor inhibitory peptide P143.
                                                                                                                                                                                                                                    08-NOV-2000
                                                                                                                                                                                                                                                                                                                            AAY93097 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Column 17; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recovering molecules that home to an organ or tissue, useful for identifying molecules that home to a specific organ or tissue, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
WO200031135-A1
                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identifying a tumour homing molecule by in vivo panning of a library -
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLDA 4
||||
4 SLDA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to a method of recovering molecules that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                               (first entry)
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95US-0526710.
97US-0813273.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; S
100.0%; P
ative 0;
                                                                                                                                                                                                                                                                                                                            9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 23;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to identify the presence of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                  liver;
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RESULT 15
AAB99639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in viro which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.
                                                                                                              Homo sapiens.
Synthetic.
                                                                                                                                                           gastritis;
                                                                                                                                                                                     rheumatoid arthritis; myasthenia gravis; systemic lupus erythematosis; chronic inflammation; atherosclerosis; inflammatory bowel disease;
                                                                                                                                                                                                                  antirheumatic; nootropic; antiarteriosclerotic; antimicrobial; antiulcer;
neuroprotective; autoimmune disease; diabetes; multiple sclerosis;
                                                                                                                                                                                                                                              Human; heat shock protein; hsp60; inhibition; antagonist; antiallergic; pro-inflammatory immune response; immune system; inflammatory disease; immunostimulatory; antiinflammatory; antidiabetic; immunosuppressive;
                                                                                                                                                                                                                                                                                                          Human hsp60
                                                                                                                                                                                                                                                                                                                                       04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                AAB99639 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ezquerro Saenz
Borras Cuesta F
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                                                                                    WO200143691-A2
                                                                                                                                                                          reactive arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides that antagonize binding of transforming growth factor betal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-411935/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SLDA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treatment of liver disease, l sequences of the factor or its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                            ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page
                                                                                                                                                                                                                                                                                                        derived peptide #65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; 86pp;
                                                                                                                                                            thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lasarte Sagastibelza JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18;
Pred. No.
                                                                                                                                                           allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                           graft rejection; gingivitis; acute infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               especially cirrhosis, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 7.8e+05; thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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15-DEC-1999;

99EP-0125035.

14-DEC-2000; 2000WO-IL00833

21-JUN-2001

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RESULT 16
AAR72570
ID AAR72
XX
AAR72570
AC AAR72
XX
DT 23-N(
XX
Peni
KW Peni
KW Peni
KW Penj
XX
PON
O7-
23-
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PD 07-
PD 07-
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PR 23-
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PR 23-
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PR 23-
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PR WP
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PR WP
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PR WP
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PR WP
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PS D:
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Disclosure; Page 7; 8pp; Japanese
                                                                                                                                                  23-AUG-1993;
                                    inulo-oligosaccharides
                                                                                                                (MITK ) MITSUI TOATSU CHEM INC
                                                                                                                                                                                                                                                JP07059574-A
                                                                                                                                                                                                                                                                         Penicillium purpurogenum
                                                                                                                                                                                                                                                                                                 Penicillium purpurogenum variety rubrisclerotium; endo-inulinase; inulo-oligosaccharides; inulin; peptide fragment 175-184.
                                                                                                                                                                                                                                                                                                                                                Penicillium purpurogenum endo-inulinase peptide fragment 175-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR72570 standard; Peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive, nootropic, antiarteriosclerotic, antinicrobial, antiluleer, antiallergic and neuroprotective activities. The antagonists are useful in the treatment of an inflammatory disease or disorder, e.g. an autoimmune disease, diabetes, multiple sclerosis, rheumatoid arthritis, myasthenia gravis, systemic lupus erythematosis, chronic inflammation, atherosclerosis, inflammatory bowel disease, reactive arthritis, chronic infections, graft rejection, glngivitis, gastritis, ulcer, thrombosis, allergy and acute infections. AAH43896 to AAH43899 and AAB99542 to AAB99673 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes anti-inflammatory peptides of heat shock protein hsp60, which are capable of acting as antagonists of hsp60 characterised by their ability to reduce or prevent the induction of a pro-inflammatory immune response of cells of the innate immune system by hsp60. The peptides have antiinflammatory, antidiabetic, antirheumatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-inflammatory peptides of hsp60, which are capable of acting as antagonists of hsp60, useful for treating an inflammatory disease or disorder, e.g. an autoimmune disease, diabetes, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kolb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Page 58; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-390150/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                DNA encoding endo-inulinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                93JP-0229448.
                                                                                                                                                                              93JP-0229448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 22; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                useful
                                          for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
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RESULT 17
AAW61058
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XCCCX
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Best Local S
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                                         AAW61058-60 represent partial amino lacid sequence of different immunoglobulin (Ig) molecules. The specification describes a non-naturally occurring IgG having an altered amino acid sequence compared to native IgG, which binds to FGRN with increased or decreased affinity. FCRn is a receptor found on the intestinal surface of the neonate and is responsible passage of maternal milk IgG from the intestinal lumen to the systemic circulation via the intestinal epithelial cells. FCRn is also used to prevent clearance of circulating IgG from the circulation. Altering the binding site on an IgG for FCRn allows greater or lower affinity for the FCRn receptor, which subsequently increases or decreases the half-life of circulating IgG, respectively. IgG's with an increased half-life can be used to treat immune conditions or diseases such as iddopathic thrombocytopaenic
                          dermatomyositis.
                                     immune conditions or diseases suc
purpura (ITP), Kawasaki disease,
                                                                                                                                                                                                                                                                            New antibody having altered Fc receptor binding site -
increased or decreased half-lives and clearance rates,
e.g. tumour imaging or treatment of AIDS
                                                                                                                                                                                                                                                    Disclosure; Fig 2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                     Israel EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09823289-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                               (UYBR-) UNIV BRANDEIS.
                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawasaki disease; AIDS; Guillain-Barre syndrome; dermatomyositis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW61058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW61058 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR72567-R72575 are peptide fragments of AAR72566, the Penicillium purpurogenum variety rubrisclerotium endo-inulinase. The endo-inulican be used to prepare an inulo-oligosaccharide from inulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                     Simister NE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            idiopathic thrombocytopaenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IgG;
                                                                                                                                                                                                                                                  32pp; English.
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Pred
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                                   AIDS,
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                                  Guillain-Barre syndrome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purpura;
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L.5e+02;
s 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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Query Match Best Local Similarity

100.0%;

Score 18; Pred. No.

DB 19; 1.5e+02;

Length

Sequence

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AA;

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RESULT 19
AAY92947
ID AAY92
XX
AC AAY92
XX
DT 08-NC
XX
DE Trans
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KW Hepat
KW compe
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AAG86956
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
Hepatotropic; antagonist; transforming growth factor betal; TGF-b1; competitive inhibition; collagen synthesis stimulation inhibitor; liver;
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200142276-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae; drug discovery; drug design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG86956 standard; Peptide; 10 AA
                                    Transforming growth factor inhibitory peptide #3
                                                               08-NOV-2000
                                                                                        AAY92947;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying complementary peptides by nucleotide sequence databases, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-367863/38
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                                                                                                              AAY92947 standard; peptide; 12 AA
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nes 4; Conserv
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                                                               (first entry)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            analysis of protein in drug design -
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                                                                                                                                                                                                                            DB 22;
1.5e+02;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY29345-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of inverdisease encoding the peptides are used for treatment of
                                                                                                                                  Rattus sp.
                                                                                                                                                           Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                        AAY93007;
                                                                                                                                                                                                                                                                                                  AAY93007 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partial sequences of the factor or its receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides that antagonize binding of transforming guseful for treatment of liver disease, especially
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                        24-NOV-1998;
                                                  23-NOV-1999;
                                                                             02-JUN-2000
                                                                                                        WO200031135-A1
                                                                                                                                                                                                                  Transforming growth factor inhibitory peptide P53
                                                                                                                                                                                                                                             08-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ezquerro Saenz IJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liver disease, specifically cirrhosis.
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                                                  99WO-ES00375
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                        98ES-0002465
                                                                                                                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                             entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
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(CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

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RESULT 21
AAY93008
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Disclosure; Page 27; 86pp; Spanish.
                              Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors
                                                                                                                                       Ezquerro Saenz
Borras Cuesta I
                                                                                                                                                                                                                                                                                                                                                                                   Hepatotropic; antagonist; transforming growth factor betal; TGF-b1; competitive inhibition; collagen synthesis stimulation inhibitor; lextracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors. e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.
                                                                                                                                                                                          (CIEN-)
                                                                                                                                                                                                                            24-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           partial sequences of the factor or its receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borras
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||SLDA
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Conservative (
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F;
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                                                                                                                                                     Sagastibelza JJ,
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0; Mismatches
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,. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                     inhibitor; liver;
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invention relates to

synthetic peptides that antagonise the binding

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RESULT 22
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                                  The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of
                                                                                                                                                                                                                 Disclosure; Page 27; 86pp; Spanish.
                                                                                                                                                                                                                                                          Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are
                                                                                                                                                                                                                                                                                                                                               Ezquerro Saenz IJ,
Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.
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                        ssion systems) encoding the peptides are used disease, specifically cirrhosis.
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AAY93093
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Best Local Similarity
                                                                                                                                                                                                                           The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibitors of stimulation of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors -
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             AAW69624 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 31; 86pp; Spanish.
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Borras Cuesta F;
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                                                                                                                                                           100.0%;
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Pred. No. 1.9e+02;
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Pred. No. 1.9e+02;
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RESULT 25 AAW74421

AAW74421 standard;

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10-MAY-1999 AAW74421;

(first entry)

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Best Local
                                                                                                                                                                                                                                                                                                                        a function naturally performed by the corresponding yeast pheromone system protein; and (b) a second heterologous gene encoding a heterologous peptide, where the heterologous peptide modulates the interaction of the surrogate with the pheromone system in the yeast cell, and the modulation is a selectable or screenable event. The yeast cells are used in assaying a peptide for modulation of the activity of a non-yeast surrogate for a pheromone system protein and determining by detecting a change in the selectable or screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable or screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the pheromone is the selectable of screenable event whether the selectable is the selectable of screenable event whether the selectable is the selectable of screenable event whether the selectable is the selectable of screenable event whether the selectable is the selectable of screenable event whether the selectable is the selectable event whether the selectable is the selectable in the select
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                    of the present invention.
                                                                                                                                                                                                                                                          pheromone signal pathway is activated or inhibited by the interaction the surrogate and the peptide. The present sequence represents an Ste2 agonist from the alpha-Mid-5 library which is from an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in which the cell comprises: (a) a first heterologous gene encoding a heterologous surrogate of a yeast pheromone system protein, the surrogate being a kinase and performing in the pheromone system of the yeast cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant yeast cells - containing gene encoding system protein surrogate and gene encoding peptide
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N-PSDB; AAV40413.
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20-SEP-1994;
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31-MAR-1993;
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                                          1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes a yeast cell having a pheromone system,
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                                                                                         Similarity 4; Conserv
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93US-0041431.
94US-0190328.
94US-0309313.
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Pred. No.
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RESULT 26
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31-JAN-1994;
20-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an Ste2 agonist peptide sequence. The invention relates to Yeast cells engineered to express an exogenous protein capable of substituting for a yeast protein involved in the post-translational modification, transport, recognition or signal transduction of a yeast pheromone. The system can be used to identify drugs which inhibit or activate the ability of the surrogate to substitute for the cognate yeast pheromone system protein. Inhibitors of farnesyl transferase identified can be used for anticancer therapies.
                                           Saccharomyces Synthetic.
US6100042-A
                                                                                                                                   Yeast; pheromone; alpha-factor; transporter; pheromone receptor; G alpha subunit; MF alpha 1; MFa1; STE2; STE3; C5a receptor; GPA G protein coupled receptor; mutagenesis; amplification; screeninhybrid; agonist; antagonist; signal transduction; detection;
                                                                                                                                                                                                                                                                  Alpha-Mid-5 library Ste2 agonist peptide sequence
                                                                                                                                                                                                                                                                                                                     21-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                     AAB20756;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB20756 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Column 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast cells having an engineered pheromone system identifying drugs which can inhibit or activate plyorotein, e.g. to develop anti-cancer therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5876951-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast pheromone; Ste2 farnesyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CADU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-189631/16.
DB; AAX18211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CADUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 М2
                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                         cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0041431.
94US-0190328.
94US-0309313.
94US-0322137.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agonist; cognate yeast pheromone system protein anticancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manfredi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pheromone system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 13;
                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                     IJ
                                                                                                                                                               screening;
                                                                                                                                                                                                                                                                     NO:96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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δÃ
                                                                                                       The present invention describes recombinant yeast cell mixtures (I). CC Each (I) has a heterologous G protein coupled receptor (GPCR) expressed cc in the cell membrane such that signal transduction (ST) activity via CFCR is modulated by interaction of extracellular region (ER) of GPCR with a heterologous polypeptide (P) which interacts with ER of receptor. CC Modulation of the ST activity by (P) provides a detectable signal. CC Also described is a recombinant yeast cell (II) that has a cell membrane cc which comprises a GPCR such that ST activity via GPCR is modulated by interaction of an ER of GPCR with an extracellular signal, and a (P) which is transported to a location allowing interaction with ER of GPCR. CC (I) is used for identifying a modulator of (P) expressed by the yeast cell which involves providing (I) which comprises heterologous GPCR and a heterologous test polypeptide, allowing the cells within the mixture to generate a detectable signal and then identifying the heterologous cest peptide as a modulator of the heterologous receptor protein cc expressed by the yeast cell. The yeast cells may be used to identify of the surrogate to substitute for the cognate yeast pheromone system contains. The yeast cell is also used to screen agonists and an analysists. The present sequence is used in the exemplification of
                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1993;
31-JAN-1994;
20-SEP-1994;
                                                                                                                                    antagonists. The prese
the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mixture of recombinant yeast cells comprising a heterologous G pure coupled receptor whose signal transduction activity is modulated transduction activity is modulated which provides a detectable signal on the contraction.
                                                                                                       Sequence
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                                  Local Similarity hes 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-531665/48
                                                                                                       13
                                  100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Broach
                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHARM
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94US-0190328.
94US-0309313.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein
                                  0,
                                                    Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy
                                                      2e+02;
                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑJ,
                                  0
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                                                                 Length 13;
                                    Indels
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                                  0;
                                    Gaps
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RESULT 27
AAG79149
AAG79149 standard;
                                    1 SLDA 4
|||||
5 SLDA 8
peptide;
13
AA.
                                                                   0;
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В

Amino acid 03-JAN-2002

(first

entry)

Cellular receptor; ion channel; cellular activity; drug discovery;

alpha-factor pheromone

of an alpha-factor pheromone

receptor ligand; sequence

US2001026926-A1

Synthetic orphan

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RESULT 28
AAB84497
В
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                           The specification describes an assay for screening and identifying pharmaceutically effective compounds that specifically interact with and modulate the activity of a cellular receptor or ion channel. The assay uses a mixture of recombinant cells, each comprising a receptor protein whose signal transduction activity is modulated by an interaction with an extracellular signal, a recombinant gene encoding a potential receptor polypeptide, and a reporter gene construct. The assay is useful for rapid screening of large numbers of polypeptides to identify polypeptides antagonizing or agonizing receptor activity, and to identify drugs for modulating cellular activity. It is especially useful to identify ligands for orphan receptors, especially ligands for orphan cell surface receptors, which are useful in drug discovery. The present sequence represents an alpha-factor pheromone agonist, which was identified using the assay of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-SEP-1994;
13-OCT-1994;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
03-JUL-2001
                                                                             surrogate ligand;
                                                                                                                  Amino acid
                                                                                                                                            05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 31; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification of compounds modulating cellular receptor activity useful for identifying and screening for ligands for orphan receptors, comprises using recombinant cells comprising both receptors and test polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-1996;
31-MAR-1993;
                          US6255059-B1
                                                 Synthetic
                                                                                                                                                                                               AAB84497 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trueheart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-1994;
                                                                                        protein
                                                                                                                                                                                                                                                                               1 SLDA 4
                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-615870/71.
DB; AAI65730.
                                                                                                                                                                                                                                                                 SLDA
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                                                                                                                                                                                                                                                                                                                    4:
                                                                                      coupled
                                                                                                               sequence of a Ste2 agonist from alpha-Mid-5 library.
                                                                                                                                                                                                                                                                                                                                                                        <u>1</u>3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy AJ,
                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0747774.
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95US-0461383.
95US-0461598.
95US-0463181.
95US-0464531.
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94US-0309313.
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93US-0041431.
                                                                       receptor; GPCR; cellular receptor;
orphan receptor; Ste2 agonist.
                                                                                                                                                                                             peptide;
                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fowlkes DM,
                                                                                                                                                                                                                                                                                                                 Score 18; DB 22
Pred. No. 2e+02;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broach J,
                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                          Length 13;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                        ion channel;
                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 29
AAY92950
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1993;
31-JAN-1994;
20-SEP-1994;
13-OCT-1994;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a method for identifying a ligand for an orphan G protein coupled receptor (GPCR). The method comprises rapidly screening large numbers of polypeptides in a yeast expression library to identify those polypeptides which induce or antagonise receptor bioactivity. The method is useful for screening and identifying pharmaceutically effective compounds that specifically interact with and modulate the activity of a cellular receptor or ion channel. The assay is particularly amenable for identifying surrogate ligands for orphan receptors. The present sequence represents a Ste2 agonist, identified from an alpha-Mid-5 library, using the method of the
                                                                                 23-NOV-1999;
                                                                                                                                                                                           Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; l
                                                                                                                                                                                                                              Transforming growth factor inhibitory peptide
                                                                                                                                                                                                                                                                                                      AAY92950 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                using
                                                          24-NOV-1998;
                                                                                                         02-JUN-2000.
                                                                                                                                WO200031135-A1
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                extracellular
                                                                                                                                                                                                                                                        08-NOV-2000
                                                                                                                                                                                                                                                                                AAY92950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Column 57-58; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a ligand for an orphan G protein coupled receptor comprises using an recombinant yeast expression library -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trueheart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-1996;
                                  (CIEN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CADU-) CADUS PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                   5 SLDA 8
                                                                                                                                                                                                                                                                                                                                                                                           1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                  INST CIENTIFICO & TECNOLOGICO NAVARRA.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                        (first
                                                                                                                                                                               nhibition; collagen synthesis stimulation
matrix degradation inhibitor; mimetope; c
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A
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94US-0190328.
94US-0309313.
94US-0322137.
95US-0463181.
                                                          98ES-0002465
                                                                                99WO-ES00375
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                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broach J,
                                                                                                                                                                                                                                                                                                                                                                                                                               2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                #6
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 13
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paul J;
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                            liver;
                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Ezquerro Saenz IJ, Borras Cuesta F;

Lasarte Sagastibelza JJ,

Prieto Valtuena

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
  The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133
                                                                                                                                                                     Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; lextracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAVGOGAE-WARTER TEPRESENT EXAMPLES OF THE PROPERTY 
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                      The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases
                                                                                                                                                       The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic nucleic acids encoding e.g. amylas oncogenes and histones, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histope; kinase; colony stimulating fact complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
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27-DEC-2000;
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2000US-0173419.
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                      The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins angiopoletin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating fact; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and cancer, autoimmune diseases and infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladde:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human peptide #755 encoded by a SNP oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM97480 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 3833; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-1999;
27-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000; 2000WO-US35498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunosuppressive; immunostimulatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grave's disease), inflammation, cancer (e.g. cancers of the bladder, in, breast, colon and kidney, leukaemia), diseases of the nervous tem and an infection of pathogenic organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-465210/50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0173419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0173419
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Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
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etes, systemic lupus erythromatosus cancer (e.g. cancers of the bladder, ukaemia), diseases of the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclins, polymerases, treating, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor;
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1 SLDA 4

Matches Query Match Best Local

Similarity 4; Conser

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RESULT 33
AAR93618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QS
                                                                                        An antigenic conjugate, useful as a vaccine for AIDS, has the formula (SpNE)n (OMPC), where SPNE is a selected principal neutralisation epitope of HIV, which is one of 27 specified polypeptides (including the present sequence) or their fragments containing at least 5 amino acids and including the DRW or DKW region; OMPC is purified outer membrane proteosome of Neisseria (pref. N. meningitidis); and n is 1-200, indicating the number of SPNE moieties covalently linked to the OMPC. The conjugates may be substituted by anions, and conjugation may be via a bigeneric spacer. The SPNE polypeptides bind an HIV broadly neutralising monoclonal antibody (2F5 antibody) specific for the ectodomain of HIV gp41 transmembrane glycoprotein. They were originally identified in the screening of phage epitope libraries having the library used was library ALPHA described in AAR83295. The sequences of these polypeptides were deduced from their corresponding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                      New antigenic conjugate useful as vaccine for AIDS principal neutralisation epitope covalently linked proteosome of Neisseria
                                                      Sequence
                                                                                                                                                                                                                                                                                                              Claim 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB2282379-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV principal neutralisation epitope binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR93618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR93618 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selected principal neutralisation epitope; vaccine; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                       BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                             Page 8; 75pp;
                                                                               determined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an infection of pathogenic organisms
                                                                                                                                                                                                                                                                                                                                                                                                                       Conley AJ,
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                                                        AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteosome; Neisseria; OMPC; AIDS; 2F5 antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
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                                                                                  PCR.
                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Kessler JA;
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Score 18; DB 10;
Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2F5 antibody.
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                                                                                                                                                                                                                                                                                                                                                     comprising HIV outer membrane
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SLDA

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RESULT 35
AAR36604
ID AAR36
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                                                                                                                                                                                             The present sequence is that of a D3 peptide derived from human CC inhibits endothelial cell proliferation and thus possesses canti-angiogenic activity. It is an example of D3 peptides of the CC invention (see AAY95405-26) that are analogues of certain sites in CC the HK domain 3, in this case amino acid residues Leu331-Tyr338, CC and in which native cysteine residues may be replaced by alanine CC and in which native cysteine residues may be replaced by alanine CC may also induce endothelial cell apoptosis. Compositions including CC the peptides are used in claimed methods for inhibiting angiogenesis, cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders contained the ICSO value for the present peptide was 42 uM for inhibition of the retina are treated. CC fibroblast growth factor-induced HUVEC cell proliferation.
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AAY95420
                                                                                                                                                    Query Match
Best Local
                                                                                                                                       Matches
       AAR36604 standard; peptide; 19
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MCCR/) MCCRAE R K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endotheliai cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-angiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-angiogenic D3 peptide
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                                                                                                                                                 Local Similarity
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                                                                                                         1 SLDA 4
                                                                               SLDA 11
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                                                                                                                                     4;
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                                                                                                                                                                                          16 AA;
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
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                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                 0;
                                                                                                                                           Score 18; DB 21;
Pred. No. 2.5e+02;
                                                                                                                                Mismatches
                                                                                                                                                       Length 16;
                                                                                                                              Indels
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AAY91397
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                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                     neuroleptic; antimanic; cerebroprotective; immunomodulatory; haemostatic; anti-microbial; cardiant; cytostatic; anti-nflammatory; haemostatic; anti-convulsant; vasotropic; vaccine; gene therapy; anti-sense therapy; neural; reproductive; immune disorder; immunodeficiency; infection; lymphoma; demyelinating disease; autoimmunity; cancer; inflammation; aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease; anti-initialization; aneurysm; haemorrhage; Alzheimer's disease;
                  aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disea
Huntington's disease; Tourette syndrome; multiple sclerosis;
ischaemia; mania; dementia; obsessive compulsive disorder;
viral prophylaxis; developmental disorder; sexually-linked di
                                                                                                                                                       Human; secreted protein; diagnosis;
                                                                                                                                                                                        Human secreted
                                                                                                                                                                                                                     29-JUN-2000
                                                                                                                                                                                                                                                   AAY91397;
                                                                                                                                                                                                                                                                            AAY91397 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See also AAR36602-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phase protein isolated from bovine serum. The protein provides a convenient marker for identifying the presence of infection prior to the onset of observable symptoms, esp. in feedlot animals. Serious illnesses may be thwarted and economic losses avoided. The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assay kit for detection and prognosis of infection and tissue damage in mammals - using acute phase proteins identified in bovine subjects suffering from infection or induced tissue damage and their specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-167625/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09309142-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminus of 37 kD acute phase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR36604;
                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                         G
                                                                                                                                                                                                                                                                                                                                                                                   1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence shown is the N-terminal sequence of a 37 kD acute se protein isolated from bovine serum. The protein provide:
                                                                                                                                                                                                                                                                                                                                                       SLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          set of observable symptoms, esp. in feedlot animals. Serious sees may be thwarted and economic losses avoided. The protein for monitering of disease states and to identify contaminated X in the sequence defines an undetermined amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 23; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redmond MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue damage; assay kit;
                                                                                                                                                                                                                  (first entry)
          disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                 protein sequence encoded by gene 23 SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0971559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92WO-CA00476
         food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harland
                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                         Scoré 18; DB
Pred; No. 3e+
0; Mismatches
                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;
                                                                                                                                                     neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marker; bovine
                                                                                                                                                                                                                                                                                                                                                                                                                         3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                    nootropic;
                                                                                                                                                                                 NO:118
                  disorder;
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preservative

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RESULT 37
AAX36691
ID AAX36691
XX AAX36
XX 17-SE
XX 17-SE
XX 17-SE
XX Humar
KW FOet:
KW autoj
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polynucleotide sequences given in AAA26281 to AAA26336 encode the human secreted proteins given in AAA91346 to AAA91449. The human secreted proteins can have activities based on the tissues and cells they are expressed in Examples of the activities are: neuroprotective; nootropic; neuroleptic; antimanic; cerebroprotective; immunomodulatory; hardiconvilsant; cardiant; cytostatic; antiinflammatory; haemostatic; anticonvulsant; and vasotropic. The polynucleotides and proteins may be used to prevent, treat or ameliorate a medical condition, e.g. by protein or gene therapy. Conditions treatable by the proteins of the invention include neural, reproductive, or immune disorders, especially immunodeficiency, infection, lymphomas, demyelinating diseases, auto-immunities, cancer, general microbial infection, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aneurysms and haemorrhages. Specific examples include: Alzheimer's disease; Parkinson's; Huntington's; Tourette syndrome; multiple sclerosis; meningitis; ischaemia; prostate cancer; mania; dementia; obsessive compulsive disorder and viral prophylaxis. The polynucleotides and proteins can also be used in the detection of disorders associated with the function of the protein, for example, the detection of developmental disorders, sexually-linked disorders, or disorders of the cardiovascular system. They may also be used as food additives or preservatives. AAA2677 to AAA2680 and AAV91345 are sequences used in
Human; secreted protein; cancer; tumour; developmental abnormality;
foetal deficiency; blood disorder; immune system disorder; inflammation;
autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 383; 416pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted proteins and corresponding DNA molecules that can be used to prevent, treat and diagnose disease in humans, for example, Alzheimer's, cancer, and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-224656/19
N-PSDB; AAA26332.
                                                                                                                  17-SEP-1999
                                                                                                                                                    AAY36691;
                                                                                                                                                                                       AAY36691 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moore PA,
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-AUG-1998;
31-AUG-1998;
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                                                                       Fragment of human secreted protein encoded by gene 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                    1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                          4;
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Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                   19 AA;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0097917.
98US-0098634.
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                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sen HS, Shi Y,
Endress GA, Ek
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 21; Length 19; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                          0,
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Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                          Indels
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AAR33356 ID AAR XX

AAR33356 standard;

peptide;

21

RESULT 38

В

14

1 SLDA 4 SLDA

0;

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CC genes. AAY36724 to AAY36727 represent the secreted protein cycles. AAY36724 to AAY36727 represent the secreted proteins encoded by chaptering genes. The genes and their corresponding secreted cyclypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a cycle can be diagnosed by determining the amount of the new polypeptides in a cycle can be diagnosed by determining the presence of mutations in the new genes. Cycle c
Matches
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carter KC, L
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 522; 537pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-418749/35.
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Yu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes encoding secreted polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1997
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18-DEC-1997;
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18-DEC-1997;
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18-DEC-1997;
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19-DEC-1997;
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                                Local
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Rosen CA, Ru
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
4.
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Greene JM,
Greene SM,
                                                                                                                           20
Conservative
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970S-0068057
970S-0068057
970S-0070923
970S-0068169
970S-0068365
970S-0068367
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97US-0068053
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970S-0068007
                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ng P, Ferrie AM, Florenc
Janat F, Kyaw H, Moore
SM, Shi Y, Soppet DR, V
0;
                                Score 18;
Pred. No.
   Mismatches
                             3.2e+02;
                                                             DB 20;
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                                                       Length 20;
   Indels
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0,
Gaps
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RESULT 39
ABB51179
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Best Local S
Matches 4
neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                  A cis-regulatory element required for virion associated protein VP16 mediated induction of herpes simplex virus 1 (HSV1) immediate early (IE) genes consists of three imperfect repeats of the purine-rich interaction with the purine-rich repeats (GA repeats) has been identified in soluble preparations of rat liver nucleic. This GA binding protein (GABP) consists of two separable subunits. Applicants have isolated cDNA clones encoding both subunits of GABP and have revealed that one (GABP alpha) is related to the Ets series of 33-amino acid repeats related in sequence to a variety
                                                                   Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
                                                                                                                              Human secreted protein encoded by gene 176 SEQ ID NO:1132
                                                                                                                                                                                                                  ABB51179 standard; Protein; 26
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding GA binding protein sub-unit - allows investigation of sub-unit sequence motif functions, for control of rapid cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CARN-) CARNEGIE INST WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09304166-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GA binding protein; cis-regulatory element; VP16 mediated induction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of tryptic peptide derived form purine-rich repeat (GA repeat) binding protien (GABP) at peale 5.
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins
                                                                                                                                                                                                                                                                                                        SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 4; 68pp;
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mc Knight
                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer
                                                                                                                                                                                                                                                                                                                                                            100
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                                                                                                                                                                                                                                                                                                                                             0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson
                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                          ; DB 14;
. 3.4e+02;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                      21;
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RESULT 40
AAU88904
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     dermatological; immunosuppressive; antinflammatory; immunostimulant; anti-HIV; cytostatic; cardiant; anti-anglogenic; ophthalmological; neuroprotective; nootropic; anti-convulsant; antilalzheimers; vascular; antiparkinsonian; antimicrobial; and vulnerary, (I) and (II) can be used in gene therapy and vaccine production, (I) and (II) can be used in the prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (BHV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiomyopathy and coronary arteriosclerosis, angiogenic chaga's cardiomyopathy and coronary arteriosclerosis, angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. tintington's chorea,
                              18-JUN-2002
                                                                                         AAU88904 standard;
                                                                                                                                                                                                                                                                                                                                                  retinopathy), neurological disorders (e.g. Huntington's Chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to ABA83193 and ABB50300 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activities based Example of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease and diabetic retinopathy - |
                                                                                                                                                                                                                                                                                                                                 the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-625724/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM,
Florence C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000;
29-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2001; 2001WO-US05614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cnaga's cardiomyopathy; coronary arteriosclerosis; anglogenic di
corneal graft neovascularisation; diabetic retinopathy; regenera
neurological disorder; Huntington's chorea; Alzheimer's disease;
Parkinson's disease; infectious disease; chromosome 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                         ω
                                                                                                                                                                                                    1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to ABB51287 and ABA83194 to ABA83441 represent human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Hu J, I
Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         er R, Lafleur DW, Moore PA, Olsen H
Soppet DR, Young PE, Shi Y, Floren
J, Hu J, Li Y, Kyaw H, Fischer CL,
                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                        Conservative
                          (first entry)
                                                                                                                                                                                                                                                                                                                                              ABB50300 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-184836P.
2000US-193170P.
                                                                                                                                                                                                                                                                                                    AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide (II) sequences. (I) and (II) have various on the tissues and cells the genes are expressed in activities include: immunomodulatory; antisclerotic;
                                                                                         Peptide;
                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1533pp; English.
                                                                                         26
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                 Score 18; DB
Pred. No. 4.2
); Mismatches
                                                                                                                                                                                                                                   4.2e+02;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y, Florence KA, Wel.
TL, Ferrie AM,
                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                      exemplification of
                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                               Gaps
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Insulin/insulin-like growth factor receptor-binding peptide #860.

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RESULT 41
AAW10854
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                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating agrowth factor (IGF-1) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1; IGF-1; tumour; prostate; breast; insulin-tic retinopathy; neurological diseases; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic neuropathy.
Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 1K-1; 390pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beasley J, 1
Brissette R,
                                                                                                                        07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating insulin activity in mammalian cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2000; 2000WO-US08528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2000; 2000WO-US08528
                                                                                                                                                     AAW10854
                                                                                                                                                                                AAW10854 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes and insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DGIB-) DGI BIOTECHNOLOGIES LLC.
                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                    1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                           the invention.
                                                                                                                                                                                                                                                          SLDA
                                                                                                                                                                                                                                                                                                                   4.
                                                                                                                                                                                                                                                                                                                                                                              26 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blume AJ,
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth factor receptors
                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lume AJ, Schaeffer
Spetzler J, Cheng
                                                                                        binder sequence,
                                                                                                                                                                                                                                                                                                                100.0%; S
100.0%; F
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hsiao
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                                                                                                                                                                                                                                                                                                                Score 18; DB 23;
Pred. No. 4.2e+02;
; Mismatches 0;
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                                                                                         FC11,
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Ostergaard S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptides that bind to i
                                                                                         from R26 library.
                                                                                                                                                                                                                                                                                                                                            Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brandt
                                                                                                                                                                                                                                                                                                                   Indels
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insulin or
                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                   Gaps
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prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                        WO9641172-A1
                                                                                                                                                                                                                           (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                             19-DEC-1996.
                                                                                                                                                                                                                                       95US-0476375
                                                                                                                                                                                                                                                  96WO-US10498
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Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules ferritin

WPI; 1997-077284/07

Claim Page 95; 156pp; English.

This sequence represents a monoclonal anti-hepatitis B antigen binder consequence from the R26 library which may be used in the conjugate of the convention. The novel labelled conjugate comprises at least one label cattached to a functional surrogate comprises at least one label cattached to a functional surrogate of an analyte of interest. The conjugate is capable of competing effectively with the analyte for a climiting amount of an affinity receptor for the analyte. The conjugate comprists an activity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules such as polypeptides, polysaccharides, polynucleotides, glycoproteins and competitive analytes for detection include cardiac or tumour markers, allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human placental confortion gonadotropin, human luteinisting hormone, human placental confortions gonadotropin, human luteinisting hormone, cytomegalovirus, DK.MB. Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour mar) (a tumour marker).

Sequence 29 AA;

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RESULT 42
AAR71050
ID AAR71
XX
AC AAR71
XX
AC AAR71
XX
DT 15-NC
XX
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                                                                                                       Matches
                                                                                                                     Query Match
                      AAR71050;
                                    AAR71050 standard;
                                                                         10
                                                                                                              Local
                                                                                        1 SLDA 4
                                                                         SLDA 13
                                                                                                      Similarity 4; Conserv
                                                                                                       Conservative
                                    Peptide;
                                                                                                             100.0%;
                                     30
                                                                                                       0;
                                                                                                              Score 18;
Pred. No.
                                      8
                                                                                                       Mismatches
                                                                                                              4.8e+02;
                                                                                                                      DB 18;
                                                                                                       0
                                                                                                                     Length 29;
                                                                                                       0;
                                                                                                      Gaps
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0;

15-NOV-1995

(first entry)

Draculin

peptide

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XXWXEXTXCXI
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                                                                                                                                                                                                                                                                                                                             RESULT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
              Clostridium perfringens food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the blood coagulation cascade. The anticoagulant activity is not inhibited by serine protease inhibitors such as PMFS or DFP. The molecular weight of Draculin ranges from 75-90 kD and may be used in treatment of acute myocardial infarction, deep vein thrombosis, pulmonary embolism, unstable angina, transient ischemic attacks, peripheral vascular or bypass occlusions and disseminated intravascular coagluation. These peptide fragments were derived from Draculin by cleavage with chymotrypsin and overlapping peptide fragments were compared to determine the complete amino acid sequence of Draculin.
                                                                                                 Clostridium
                                                                                                                                                       27-MAR-1998
                                                                                                                                                                                                                AAW31683
                                                                                                                                                                                                                                                              AAW31683 standard; Protein; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAR71038-84 represent peptide fragments derived from the anticoagulant protein, Draculin. Draculin is isolated from the saliva of vampire bats and is distinct from other known anticoagulants in that it inhibits both factors IX and X of the limit of the li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anticoagulant protein, draculin, from vampire bat saliva and related nucleic acid, vectors, transformed cells and probes, for treating myocardial infarction, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anticoagulant; Draculin; saliva; vampire bat; inhibition; factor IX; factor X; blood coagulation cascade; serine protease inhibitor; PMFS; acute myocardial infarction; deep vein thrombosis; pulmonary embolism; unstable angina; transient ischemic attack; peripheral vascular; DFP; bypass occlusion; disseminated intravascular coagluation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; Page 34; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-106668/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apitz-Castro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RHON ) RHONE POULENC RORER PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desmodus rotundus
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                                                                                                                                                                                                                                                                                                                                                                                                          SLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                        perfringens type A enterotoxin
                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bequin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Undefined amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
                                        type A enterotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0%; Score 18; DB 1b; 
).0%; Pred. No. 4.9e+02; 
^. wismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hemker HC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holt JC,
                                                                                        (residues 291-319).
                                  toxoid; vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lynch K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 44
AAY95418
ID AAY95
XX
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                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence corresponds to a carboxy-terminal protein fragment (amino acid residues 290-319) of the Clostridium perfringens type A enterotoxin protein. Plasmids containing E. coli expression vectors and Clostridium perfringens type A enterotoxin gene fragment encoding amino acid residues 171-319 or 290-319 can be used to produce Clostridium perfringens type A enterotoxin toxoids. A synthetic peptide corresponding to these residues 290-319 can also be prepared to be used as a toxoid. These toxoids irreversibly bind to and saturate receptor sites on intestinal membranes, thus effectively competing for these receptor sites with Clostridium perfringens type A enterotoxin. The synthetic peptide and the recombinant carboxy-terminal fragment, are useful as toxoids in a vaccine for preventing C. perfringens food poisoning, or in a
                                                                                                                            Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide; cyclic.
16-DEC-1998;
                         02-DEC-1999;
                                                   22-JUN-2000
                                                                            WO200035407-A2
                                                                                                      Homo sapiens
                                                                                                                                                                                            Anti-angiogenic D3 peptide.
                                                                                                                                                                                                                       25-SEP-2000
                                                                                                                                                                                                                                                 AAY95418;
                                                                                                                                                                                                                                                                     AAY95418 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Columns 19-20; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA molecule encoding Clostridium perfringens enterotoxin fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium perfringens. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYPI-) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-1990;
22-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                       1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxoid in vaccine for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                          30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcclane BA,
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                    (first entry)
                        99WO-US28465
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92US-0874982.
94US-0213452.
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                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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2
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AX Funct
KW Funct
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                                                                                                                                                                                                                                                     Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain
Carter JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                             MAb anti-HBsAg binder sequence, FC11, from R26 library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW10869 standard; peptide; 33 AA
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                                                                         07-JUN-1995;
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                                                                                                                                                                                                                      Synthetic.
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Pred. No. 5.3e+02;
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14 SLDA 17

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Search completed: February Job time: 29.8333 secs

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CC limiting amount of an affinity receptor for the analyte. The conjugate CC exhibits an activity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have CC an immunoreactive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor. CC Functional surrogates are able to mimic naturally occurring analytes. CC (esp. homogenous immunoassays) for detecting large macromolecules such CC as polypeptides, polypactoles, as well as small haptens. Typical CC diagnostic analytes for detection include cardiac or tumour markers, CC allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for CC detecting ferrith, follicle stimulating hormone, human growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human growth hormone, CC chamoglobulin E, prolactin, parathyroid hormone, cytomegalovirus, CC chamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, CC alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surrogate is capable of competing effectively with the analyte for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a monoclonal anti-hepatitis B antigen binder sequence from the R26 library which may be used in the conjugate of tinvention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 51; Page 100; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               such as ferritin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-426-568A-10
US-08-426-855-12
US-09-226-985-12
US-09-227-906-12
US-08-461-598-96
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US-08-322-137-96
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US-08-322-131-119
US-08-213-452-3
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US-08-313-9012-130
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48, Appl
53, Appl
10, Appl
112, Appl
112, Appl
112, Appl
112, Appl
113, Appl
130, Appl
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1 SLDA |||| 2 SLDA

Query Match Best Local Si Matches 4;	RESULT 1 US-08-136-743B-48 Sequence 48, Application US/08136743B Sequence 48, Application US/08136743B Sequence 48, Application US/08136743B Sequence 48, Application US/08136743B Patent No. 5459063 GENERAL INFORMATION: APPLICANT: BAITY S. Cooperman, Ha APPLICANT: Jerome Salem, and Alis TITLE OF INVENTION: Clectide Redu TITLE OF INVENTION: Thereof "Plasmodium for Inversity of Plasmodium of Inversity of Inve		28 30 31 31 31 32 33 33 33 34 35 36 37 38 38 39 39 39 18 40 41 42 18 42 18 18 18 18 18 18 18 18 18 18
100.0 Similarity 100.0 4; Conservative	136-743B-48 EERAL INFORMATION: PPLICANT: Barry S. Cooperman PPLICANT: Jerome Salem, and ITLE OF INVENTION: Thereof "Plasmodi ITLE OF INVENTION STREET: 3700 Market Street CITY: Philadelphia STATE: Philadelphia COUNTRY: U.S.A. ZIP: 19104-3246 COMPUTER: BADABLE FORM: MEDIUM TYPE: Diskette, 3.50 COMPUTER: IBM PS/2 OPPERATION SYSTEM: MS-DOS SOFTWARE: WORDER: US/08/1 FILLE MONACO, DATA: APPLICATION UNMBER: US/08/1 FILLE MONACO, DATA: APPLICATION UNMBER: 39 CLASSIFICATION INFORMATION: NAME: MONACO, DATA: REFERENCE/DOCKET NUMBER: 39 PLECOMMUNICATION INFORMATION: REFERENCE/DOCKET NUMBER: 39 REFERENCE/DOCKET NUMBER: 39 REFERENCE/DOCKET NUMBER: 30 REFE		100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0
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; Score 18; DB 1; ; Pred. NO. 1.9e+05; 0; Mismatches 0;	rvey Rubin. on L. Fisha alciparum ctase, DNA nnsylvania nn, 720 Kb	ALIGNMENTS	US-08-936-165A-515 US-09-099-041A-6 US-09-199-637A-231 US-09-245-281-6 US-09-247-359B-6 US-09-437-054A-2 US-08-461-511A-19 US-08-461-511A-9 US-08-461-511A-8
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RESULT 4
US-09-426-568A-10
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US-09-001-984C-53
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-1
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/001,984C
CURRENT FILING DATE: 1997-12-31
                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/040,216 CURRENT FILING DATE: 1998-03-17 EARLIER APPLICATION NUMBER: 08/919,748 EARLIER FILING DATE: 1997-08-28 EARLIER APPLICATION NUMBER: 60/025,146 EARLIER FILING DATE: 1996-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS TITLE OF INVENTION: SMALL MOLECULES USEFUL FOR INHIBITING THE TITLE OF INVENTION: RIBONUCLEOTIDE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 61 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                            ILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 9596-63U
                                                                                                                                                                                                                                  ENGTH:
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                                                                                                                       Conservative
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                                                                                                                                            Length 7;
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                                                                                                 SOFTWARE: Patentin Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 11-SEP-199)
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 008
                            REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
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                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                STREET: 4,,
STREET: San Diego
CITY: San Diego
CMATE: California
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                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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APPLICANT: Pasqualini,
TITLE OF INVENTION: Met
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LOCATION: (1)..(7)
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TYPE: PRT
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             TELEPHONE:
                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                      COUNTRY: UZIP: 92122
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o. 6348643
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· (619)
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                    United States
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Hu, Weiming
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                                                                                                                                                                                                                                                                                                                                                                                                                            Ruoslahti, Erkki
             (619) 535-9001
                                                                                                                       11-SEP-1995
                                                                                                                                                                                                                  Floppy disk
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008103/195497
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Method of
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Colleen
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                                                        31,815
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Pred! No. 1.9e+05;
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Patent No. 6068829
GENERAL INFORMATION:
                                                      Matches
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Best Local
                                                                                Query Match
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INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENCTH: 8 amino acids
TYPE: amino acid
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,710
FILING DATE: 11-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/813,273
FILING DATE: 10-MAR-1997
ATTONNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 2621
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
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CURRENT APPLICATION DATA:
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                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
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4370 La Jolla Village Drive, Suite 700
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                                                                                                                                          linear
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                                                  Score 18; DB 3; Pred. No. 1.9e+05;
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Pred. No.
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US-09-227-906-12
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                                                                                                                                                                                                      GENERAL INFORMATION:
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                       APPLICANT: Ruoslahti, Erkki APPLICANT: Pasqualini, Rena TITLE OF INVENTION: Method TITLE OF INVENTION: Home to NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 01 FILING DATE: 11-SEP-1995 PRIOR APPLICATION DATA:
STREET: STREET STREET SAN Diego CITY: San Diego California
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APPLICATION NUMBER:
                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/226,985 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4370 La
CITY: San Diego
STATE: Californi
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                                                        E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
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4370 La Jolla Village Drive, Suite 700
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ilarity 100.0%;
Conservative 0
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                                                                                                                              Method of Identifying Molecules That Home to a Selected Organ In Vivo
                                                                                                                                                 Method of
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Pred. No.
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READABLE FORM:

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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APPLICANT:
APPLICANT:
                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                     APPLICANT: TRUEHEART, JOSHUA
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,710
FILING DATE: 11-SEP-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 01
FILING DATE: 23-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/813,273
FILING DATE: 10-MAR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                         STREET: 419 Seven
APPLICATION NUMBER: US/08 FILING DATE: 05-JUN-1995
                                                                                                                                      COUNTRY: UZIP: 20004
                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08464531
                                                                                                                                                                                                  419 Seventh Street, N.W., Suite 300
                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 amino acids
                                                                                                                                                                                                                                                                                                                    MURPHY, Andrew J. PAUL, Jeremy
                                                                                                                                                                                                                                                                                                                                                   KLEIN, Christine
                                                                                                                                                                                                                                                                                                                                                                     MANFREDI, John
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                                                                                                                                                                                                                                                                                                                                                                                                    FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                     BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 18;
100.0%; Pred. No. 1
                 US/08/464,531
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                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 58/00.
Patent No. 58/00.
Patent No. 58/00.
Patent No. 58/00.
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Best Local Similarity
                                                                                                                                                                                                                                                            APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, JOSHUA
APPLICANT: TRUEHEART, JOSHUA
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES,

""""" OF SEQUENCES: 119
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                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: FOI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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LENGTH: 13 amino acids
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FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/322,137 FILING DATE: 13-OCT-1994
                                                          APPLICATION NUMBER: US/08/461,598 FILING DATE: 05-JUN-1995
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                 COUNTRY:
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419 Seventh Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                               John
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Pred, No. 51;
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PRIOR APPLICATION DATA:

US 08/190,328

APPLICATION NUMBER: US 08/309,313 FILING DATE: 20-SEP-1994

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;; TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-461-598-96
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US-08-322-137-96
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                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/322,137
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
PRICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 13 amino acids
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REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: YEAST CELLS ENGI
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ZIP: 200
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                                               APPLICATION NUMBER: US 0 FILING DATE: 31-JAN-1994
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                    TRUEHEART, JOShua
VENTION: YEAST CELLS ENGINEERED TO PRODUCE
VENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
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31-MAR-1993
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"BER: FOLWKES-2F
                                                               US 08/190,328
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Matches
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Matches
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                                                            Query Match
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APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Identifying Receptor Effectors
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-4214
INFORMATION FOR SEQ ID NO: 32:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Catherine J. Kara
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,3
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
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                                                                                                             MOLECULE TYPE:
                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
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                                               Local Similarity
                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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1 SLDA 4
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nilarity 100.0%;
Conservative 0
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                                               Score 18; DB Pred. No. 51;
                               Mismatches
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                                                              4.
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                               Indels
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US-08-887-534A-94
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Best Local Similarity
Watches 4; Conserve
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                                                                                                                                                                                                                  RESULT 14
                                                                                                                                              Patent No. 6455323
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5695956
GENERAL INFORMATION:
APPLICANT: McClan
                                                                                                                                                                  Sequence 94, Application US/08887534A Patent No. 6455323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORIGINAL TOPOCHTOION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOULD, JT., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                              APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lewis F. Gould, Jr. STREET: 1700 Market St. Suite 3232 CITY: Philadelphia
                                               STREET:
                                                                                                                                                                                                                                                                                   1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
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                                                                  ADDRESSEE:
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                                   Chicago
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               Illinois
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                                               E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive/6300 Sears Tower
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Mietzner, Timothy A.
Mietzner, Timothy A.
VENTION: Clostriddium perfringens Type A
VENTION: Enterotoxin Toxoid and Methods of Preparation and Use As
VENTION: Vaccine and Therapeutic Agent
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                                                                                                                                                                                                                                                                                                                                  Conservative
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States of America
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                                                                                                  106
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Pred. No. 1
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                                                                                                                AND MATERIALS
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Best Local Similarity
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TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/209,521
APPLICATION NUMBER: US/08/209,521
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
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                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
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MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS!
SOFTWARE: Patentin Release #1.0; Version #1.30
CURRENT APPLICATION DATA:
                                                             REFERENCE/DOCKET NUMBER: OHSU 306A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 63 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 520 S.W. CITY: Portland
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack & ADDRESSEE: Heuser
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Y: US
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Bronner, C. Eric
Baker, Sean M.
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   295-6679
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                                  224-6655
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US-08-209-521-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Liskay
                                                                                                                                                                                                TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
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TITLE OF INVENTION: hMLH1 AND hPMS1
NUMBER OF SEQUENCES: 30
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                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/209,521 FILING DATE: 08-MAR-1994
24 SLDA 27
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                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 97204
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                                                                                                                                                                                    64 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker, Sean M.
Bollag, Roni J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear
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                                                                                                                                              linear
                                                                                                                                                                                                                                             (503) 224-6655
                                                                                                                                                        single
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MAMMALIAN DNA MISMATCH REPAIR GENES
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Pred. No. 2.9e+02;
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Pred. No.
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                                                       2.9e+02;
hes 0;
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RESULT 17

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US-08-961-810-130
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                                                                                                                                                                                                                                                                  RESULT 18
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US-08-961-810-129
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Liskay,
APPLICANT: Bronner
APPLICANT: Baker,
                                                                                                                                                                                                                Sequence 1:
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 129, Application US/08961810 Patent No. 6165713
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (503) 295-679
TELEX: 360619
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...ACTERISTICS:
64 amino acids
rYPE: amino acid
STRANDEDNESS: s1-
TOPOLOGY:
1. OLECULF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,810
FILING DATE:
                                                         APPLICANT: Bollag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: OH TELECOMMUNICATION INFORMATION: (503) 224-6655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHOTITLE OF INVENTION: MISMATCH REPAIR GENES NUMBER OF SEQUENCES: 134
                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                 24 SLDA 27
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
STREET: 5
STREET:
                 ADDRESSEE:
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). 6165713
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                                                                                                                                                                                                                                                                                                                                                                                     4;
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Y: U.S.A.
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E: Heuser
520 S.W. Yamhill Street, Suite 200
                                                                                                                                                Bronner, C. Eric
Baker, Sean M.
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Baker, Sean M.
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                                                                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                 Liskay, Robert M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heuser
                          Kolisch, Hartwell, Dickinson, McCormack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kolisch, Hartwell, Dickinson, McCormack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOSITIONS AND METHODS RELATING TO DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richard D.
                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OHSU 306B
                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB , pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 64;
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                                                                                                                                                                                                                                                                                                                                                                                     0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

STATE: U.S COUNTRY: U.S 77204

U.S.A.

Oregon

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TELEPHONE: (503) 224-6659
TELEFAX: (503) 295-6679
TELEX: 360619
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-810-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
US-08-352-902D-129
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GENERAL INFORMATION:
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Best Local Similarity 100.
Watches 4; Conservative
                        COUNTEL: U.S.A.
ZIP: 97204

COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,902D
FILING DATE: 09-Dec-1994
CLASSIFICATION: <UNknown>
ATTORNEY/AGENT INFORMATION:
NAME: Van RYSSelberghe, Pierre C.
REGISTRATION NUMBER: 33,557
DEFERENCE TOYCUER MITHERE. 33.65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: OH TELECOMMUNICATION INFORMATION: TELEPHONE: (503) 224-6655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 SLDA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          KOlodner, Richard D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA
MISMATCH REPAIR GENES
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liskay, Robert M.
Bronner, C. Eric
Baker, Sean M.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 149
                                                                                                                                                                                                                                                                                                                                              STREET: 520 S.W. Yamhill Street, Suite 200
                                                                                                                                                                                                                                                                                                                                   CITY: Portland
              REFERENCE/DOCKET NUMBER: OHSU 306B
                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                             STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (503) 295-6679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bollag, Roni J.
                                                                                                                                                                                                                                                                                                                                                                        Heuser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 18; DB 4; 100.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/961,810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 64;
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US-08-352-902D-130
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US-08-352-902D-130
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Ouery Match 100.0%; Score 18; DB 4; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 130, Application US/08352902p Patent No. 6191268
GENERAL INFORMATION:
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                                                                                                                                                                                                                    TELEX: 360619
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 360619
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
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                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown> |
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: 0HSU 306B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SLDA 4
                                                                                                                                                                                                                                                                                               TELEPHONE: (503) 224-6655
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release:#1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,902D
FILING DATE: 09-Dec-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOLOGNEY, RICHARD D.1
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA
NUMBER OF SEQUENCES: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liskay, Robert M.
                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                         TELEFAX: (503) 295-6679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 97204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker, Sean M.
Bollag, Roni J
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(503) 295-6679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 - 6655 -
                                        DB 4; Length 64;
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Indels

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Gaps

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1 SLDA 4 SLDA 27

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RESULT 22
US-08-798-897-16
; Sequence 16, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
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US-08-469-260A-33
                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-469-260A-33
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                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,260A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFINABLE: DESTEE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
CITY: A
                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 708-938-2623
                                                                                                                                   1 SLDA 4
                                                                                                                   58 SLDA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: POREMBSKI, PRISCILLA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
                                                                                                                                                                                                                                                                                                                 73 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
                                                                                                                                                                                 Conservative
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                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                           Score 18; DB 4;
Pred. No. 3.4e+02;
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                         Length 73;
                                                                                                                                                                               Indels
                                                                                                                                                                              0;
                                                                                                                                                                              Gaps
                                                                                                                                                                              0;
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; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: not releva
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-798-897-16 RESULT 23 US-08-978-523-16 뮍 Ω Sequence 16, Application US/08978523 Patent No. 5883229 GENERAL INFORMATION: Query Match
Best Local Similarity
Matches 4; Conserv COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC DOS/MS-DOS
SOFTWARE: PATENTE PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 13,893
REFERENCE/DOCKET NUMBER: 1483.0140001 APPLICANT: Guastella, Jo TITLE OF INVENTION: Genn TITLE OF INVENTION: HOM TITLE OF SEQUENCES: 53 CORRESPONDENCE ADDRESS: APPLICANT: Guastella, :
TITLE OF INVENTION: Ger
TITLE OF INVENTION: Hon
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS: FILING DALL.

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

APPLICATION NUMBER: February 11, 1997 ZIF: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk STATE: I APPLICATION NUMBER: UP FILING DATE: herewith CITY: Washington STATE: DC STATE: STREET: COUNTRY: 70 SLDA 73 STREET: ADDRESSEE: ADDRESSEE: 1 SLDA 4 20005 Washington : DC 1100 New York Avenue, N.W., Suite 600 1100 New York Avenue, N.W., Suite 600 USA USA Conservative Guastella, John Guastella, John STERNE, not relevant Homologue Homologue 100.0%; Genes Coding For Bcl-y, a Bcl-2 Genes Coding For Bcl-y, a Bcl-2 KESSLER, GOLDSTEIN & FOX P.L.L.C US/08/978,523 16: 0; Score 18; DB 1; Pred. No. 3.9e+02 Mismatches Version #1.30 Length 84 Indels 0 Gaps

0.

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Sequence 59, Application US/09186276B
Patent NO. 6388173
GENERAL INFORMATION:
APPLICANT: Benfey, Philip
APPLICANT: Benfey, Philip
APPLICANT: Wysocka-Diller, Joanna
APPLICANT: Wysocka-Diller, Joanna
APPLICANT: Walamy, Jocelyn E.
APPLICANT: Helariutta, Yrjo
APPLICANT: Helariutta, Yrjo
TITLE OF INVENTION: Scarecrow Gene, Promoter and Use
FILE REFERENCE: 5914-075-99
CURRENT APPLICATION NUMBER: US/09/186,276B
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
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US-09-186-276B-59
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US-09-134-001C-3985
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US-08-978-523-16
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LENGTH: 85
TYPE: PRT
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn DOUCETTE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3985, Application US/09134001C Patent No. 6380370
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 26 SLDA 29
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 SLDA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Pred. No.
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Pred. No.
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Mismatches 0;
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                                                                         Uses Thereof
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; LOCATION: (1)...(90)
; OTHER INFORMATION: Xaa =
US-09-186-276B-59
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              GENERAL INFORMATION:
APPLICANT: Benfey et al.
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 5914-074-999
CURRENT APPLICATION NUMBER: US/09/186,188B
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR FILING DATE: 1997-04-24
PRIOR FILING DATE: 1997-04-24
                                                                                                                                                                          Sequence 59, Application US/09186188B Patent No. 6455672
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LENGTH: 90
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 59
LENGTH: 90
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Best Local
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Best Local Similarity
Matches 4; Conser
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EARLIER FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/842,445A CURRENT FILING DATE: 1997-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses TITLE OF INVENTION: Thereof FILE REFERENCE: 5914-056-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Benfey et al
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PRIOR APPLICATION NUMBER: 08/638,617
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
PRIOR APPLICATION NUMBER: 08/638,617
                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT LOCATION: (1)...(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Plant
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NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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5. 6441270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FastSEQ
                                                                                                                                                                                                                                                                                                                                                    100.0%; Score'18; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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Pred. No. 4.2
0; Mismatches
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; NAME/KEY: VARIANT; LOCATION: (1)...(90); OTHER INFORMATION: Xaa - Any Amino Acid US-09-186-188B-59
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US-08-936-165A-515
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 59
LENGTH: 90
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                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.1
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION MUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: G1mm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOKET NUMBER: 950549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Plant
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ward, Judith
APPLICANT: Ward, Judith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478 TELEFAX: 610-270-5090
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                  LENGTH: 105 amino act
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-0939
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Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pratt, Julie
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Protein
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                                                                                                      515:
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Pred. No. 4.2e+02;
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; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PAT
; ORGANISM: Homo sapiens
US-09-099-041A-6
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Best Local Similarity
Thes 4; Conserve
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US-09-099-041A-6
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                                                                         US-09-199-637A-231
                                                                                                                                           PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Bertin, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09099041A Patent No. 6340576
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Best Local Similarity
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2
Patent No.
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CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
                                                                                                                                                                                                                                  APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
CURRENT FILING DATE: 1998-11-25
                                                                                                              LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                          ORGANISM: Pseudomonas aeruginosa
Local Similarity hes 4; Conserv
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o. 6355411
                                                                                                                                   109
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                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                         Tan,
                                                                                                                                                                                                                                                                                                                                                                                                            Ausubel, Frederick
Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 18; DB 4;
ilarity 100.0%; Pred. No. 5.2e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                            Man-Wah
                 100.0%; Score 18; DB 4; 100.0%; Pred. No. 5.2e+02;
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                                    Length 109;
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Matches

Conservative

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Mismatches

Indels

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Gaps

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SLDA

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CURRENT APPLICATION NUMBER: US/09/207,359B
CURRENT PILIAG DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILLING DATE: 1998-06-17
PRIOR FILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILLING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
US-09-207-359B-6
RESULT 33
US-09-437-054A-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
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                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09207359B
Patent No. 6469140
GENERAL INFORMATION:
APPLICANT: Bertin, John
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-112001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 07334/118001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                  1 SLDA 4
                                                                            29 SLDA 32
                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                        Conservative
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                                                                                                                                                                      100.0%;
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                                                                                                                                                                  Score 18; DB 4;
Pred. No. 5.3e+02;
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Pred. No. 5.2e+02;
                                                                                                                                                    Mismatches
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                                                                                                                                                                                      Length 110;
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; LOCATION: (85)
US-09-437-054A-2
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Patent No. 5834309 5710045
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LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15,
                              NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:090--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Allen, Stephen M.
APPLICANY: Kinney, Anthony J.
TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
FILE REFERENCE: BB1273 US NA
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/107,909|
PRIOR FILING DATE: 1998 No. 6316698ember-10
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                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-UN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 19
SOFTWARE: microsoft Office 97
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS |
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Thompson, Craig B. B. APPLICANT: Boise, Lawrence H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
               CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 SLDA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 5
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US-08-461-511A-15
; Sequence 15, Application US/08461511A
; Patent No. 6303331
; GENERAL INFORMATION:
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                                                                                                                                            RESULT 36
US-09-134-001C-2929
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                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-08-461-511A-15
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                                                                                                                                                                                                                        밁
               GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                        Sequence 2929, Application US/09134001C Patent No. 6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REGISTRATION NUMBER: 37,642
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                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                    1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
CTDANISTRESC: UTILITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: ARCD:179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thompson, Craig B.B.
Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            4
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STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Texas
NUMBER: US/09/134,001C
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Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                           Score 18; I
Pred. No. 5.
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                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                             .9e+02;
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                                                                                                                                                                                                                                                                                                                           Length 121;
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US-08-213-452-2
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                                                                                                                        ; MOLECULE TYPE: protein US-08-213-452-2
                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEFAX: (215) 575-6015
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2929
LENGTH: 124
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                                                                         Query Match
Best Local Similarity
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                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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120 SLDA 123
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                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                           1 SLDA 4
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VENTION: Clostridium perfringens Type A

VENTION: Clostridium perfringens Type A

VENTION: Vaccine and Therapeutic Agent
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanna, Philip C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McClane, Bruce A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis F. Gould, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                         100.0%; Score 18; DB 1; 100.0%; Pred. No. 7.4e+02;
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                                                                                                                                                                                                                                                                                               25,057
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Pred. No.
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                                                                                        Length 149;
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US-08-606-143-18
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                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/60
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO:
STREET: 550
CITY: Palo Alto
                                                                 CORRESPONDENCE ADDRESS:
                                                                                                 APPLICANT: Liu, Philip T.
TITLE OF INVENTION: LOW-T
TITLE OF INVENTION: ANALO
                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
                                                                                     UMBER OF SEQUENCES:
                                                                                                                                               APPLICANT:
                                                                                                                                                             PPLICANT:
                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                  53 SLDA 56
                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 4; Conserv
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TOPOLOGY: lir
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                                      350 Cambridge Ave., Suite
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Two Prudential Plaza, Suite 4900
                                                                                                                                                     Chung, Albert D.
                                                                                                                                                                                     Villarete,
                                                                                                                                                                                                                Subramaniam, Prem S.
                                                                                                                                            Li, Wayne W.
                                                                                                                                                                                                   Pontzer, Carol
                                                                                                                                                                                                                                Johnson, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                ANALOG
                                                                                                       LOW-TOXICITY HUMAN INTERFERON-ALPHA
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                                                                                                                                                                                     Lorelie H.
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Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 152;
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US-09-069-023-6
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                                                                   Query Match
Best Local :
                                                       Matches
                                                                                                                                                                   SOFTWARE: PatentIn
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09069023A Patent No. 6348573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/069;023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                      APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                         LENGTH: 16
TYPE: PRT
                                                                                                                          ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 27008
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/6
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
86
                                                                   Local Similarity
                          1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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SLDA
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89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hulfn-alpha analog Ifna-n6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 amino acids
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                               Score 118; DB 4,
Pred. No. 8.4e+02;
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RESULT 41

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RESULT 42
US-08-470-670A-9
; Sequence 9, Application US/
; Patent No. 5834309
; Patent No. 5834309 5710045
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                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Thompson, Craig
APPLICANT: Boise, Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Releacement APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 1938622
CLASSIFICATION: 424
CLASSIFICATION: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312-755-4489
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
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SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646008thrup, Thor
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARC
                                                                                                                                                                                                                                  TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Vertebrate Apoptosis Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thompson, Craig B. APPLICANT: Boise, Lawrence H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         74 SLDA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid TOPOLOGY: linear
                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    COUNTRY: UI
ZIP: 77210
                                                                                                                                                CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100 les 4; Conservative
                                                           MEDIUM TYPE:
                                                                                                                                     STATE:
                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SLDA 4
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                                                                                                                                     Texas
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321 No. 56
                                                                                                                                                   P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 amino acids
                                                                                                                United States of America
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                                                                                                                                                                                                                                                                                   Thompson, Craig B. B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
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5646008th Clark Street, Suite 800
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              Release #1.0, Version #1.30
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Pred. No. 8
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US-08-461-511A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-461-511A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08461511A Patent No. 6303331 GENERAL INFORMATION:
                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARCD:179

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEPHAN: (512) 474-7577

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 22-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
               MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thompson, Craig B.B.
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                                                                   LENGTH: 170 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/461,511A FILING DATE: 05-Jun-1995 CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston
                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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Pred. No. 8.5e+02;
; Mismatches 0;
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                 NO:
                 9:
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Query Match

100.0%;

Score 18;

DB 4;

Length 170;

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Sequence 8, Application US/09271014A

Patent No. 6395510

GENERAL INFORMATION:
APPLICANT: THOMESON, CRAIG B.
APPLICANT: BOISE, LAWRENCE H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:316

CURRENT APPLICATION NUMBER: US/09/271,014A

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 170

TYPE: PRT

ORGANISM: Human
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PCT-US94-07089-9
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US-09-271-014A-8
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                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07089
FILING DATE: CONCURRENTLY FILED
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/081.448
FILING DATE: 22 JUNE 193
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: AFCD090
TETITOCHAMITATION TOWNERS: ARCD090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application PC/TUS9407089 GENERAL INFORMATION:
APPLICANT:
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Best Local Similarity
Matches 4; Conserv
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                                  TELEFAX: 713-789-2679 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                       TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                         STATE: TX
COUNTRY: Un
ZIP: 77210
                                                                     TELEPHONE:
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Compositions and Methods
                                      9:
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; Pred. No. 8.5e+02;
0; Mismatches 0;
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; MOLECULE TYPE:
PCT-US94-07089-9
Search completed: February Job time: 10.3333 secs
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Best Local Similarity
Matches 4; Conserv
                                              74 SLDA 77
                                                                                                                                                              TOPOLOGY: linear
                                                                    1 SLDA 4
                                                                                          100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                 protein
        6,
          2003, 11:24:07
                                                                                          0;
                                                                                       Score 18; DB 5; 1
Pred, No. 8.5e+02;
; Mismatches 0;
                                                                                                            Length 170;
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Result
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Maximum DB
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Perfect score:
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seq length: 2000000000
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Match
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Listing first 45 summaries
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    /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
    /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
    /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
    /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
    /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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US-09-758-426-41

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3 US-09-758-128-41

3 US-09-758-128-41

3 US-09-758-128-44

4 US-09-758-128-44

5 US-09-309-196-96

6 US-09-309-196-96

6 US-09-904-615-118

6 US-09-904-615-118

6 US-09-904-615-118

6 US-09-864-761-35349

6 US-09-864-761-35349

6 US-09-727-801-8

8 US-09-727-801-8

8 US-09-864-761-34730
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15.202 Million cell updates/sec
                       Sequence 45, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 44, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 96, Appl
Sequence 118, App
Sequence 118, App
Sequence 45603, A
Sequence 54, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 14, Appl
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Sequence 181,
Sequence 267,
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	-09-86	US-09-216-393-58	US-10-105-931-6	US-09-728-721-6	US-09-975-719-231	US-10-118-984-6	US-09-939-980-515	US-09-905-243-49	US-09-905-243-48	US-09-867-550-338	US-10-014-269-21	US-10-002-974-21	US-09-841-879B-10	US-09-931-071-11	US-10-108-605-281	US-09-893-737-56	US-09-925-300-1597	US-09-764-877-1555	US-09-864-761-40746	US-09-764-877-1348	US-09-925-300-1880	US-09-764-869-1073	US-08-424-550B-33	US-09-864-761-34065	US-09-796-692-1225	US-09-864-761-46194
order or story sign	178		0	Sequence 6, Appli	Sequence 231, App	Sequence 6, Appli	515,	49,	48,	338,	Sequence 21, Appl	Sequence 21, Appl	10,	•	Sequence 281, App	Sequence 56, Appl	Sequence 1597, Ap			Sequence 1348, Ap	Sequence 1880, Ap	Sequence 1073, Ap	Sequence 33, Appl	Sequence 34065, A	Sequence 1225, Ap	Sequence 46194, A

ALIGNMENTS

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APPLICANT: ENDL, JOSEÍ
APPLICANT: STAHL, Peter
APPLICANT: ALBERT, Winfried
APPLICANT: ALBERT, Winfried
APPLICANT: BOITARD, Christian
APPLICANT: BOITARD, Christian
APPLICANT: WAN ENDERT, Peter
APPLICANT: UNG, Gunther-Gerihard
TITLE OF INVENTION: AUTOREACTIVE PETIDES FROM
TITLE OF INVENTION: DECARBOXYLASE (GAD)
FILE REFERENCE: 564-7029
CURRENT APPLICATION NUMBER: US/08/981,824
CURRENT APPLICATION NUMBER: PT.
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1996-07-15
EARLIER FILING DATE: 1995-07-15
EARLIER FILING DATE: 1995-07-15
EARLIER FILING DATE: 1995-07-14
NUMBER OF SEG ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEG ID NO 45
RESULT 2
US-09-758-426-41
: Sequence 41, Application US/09758426
: Patent No. US20020169116A1
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US-08-981-824-45
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Best Local (
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TYPE: PRT
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Pred. No. 1.1e+05;
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US-09-758-198-41
; Sequence 41, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; APPLICANT: WESTBROOK, Simon L.
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                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Rat
US-09-758-426-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF FILE REFERENCE: 016786/0214
CURRENT PAPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 09/194,218
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100 Matches 4; Conservative
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Best Local Similarity
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APPLICANT: GERRATY, No. US20020169116Alman L.

APPLICANT: WESTBROOK, Simon L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCTURES AND HORSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: AU PN9990 PRIOR FILING DATE: 1996-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020169116Alman L.
APPLICANT: WESTBROOK, Simon L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 58
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  INVENTION:
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MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
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US-09-758-198-44
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                                                                                     GENERAL INFORMATION:
APPLICANT: Kakefuda, Genichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/097 Publication No. US20020187925A1 GENERAL INFORMATION:
                                                                                                                              Sequence 10, Application UP Patent No. US20020053098A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SÖFTWARE: PatentIn Ver.
SEQ ID NO 44
LENGTH: 7
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SEQ ID NO 41
LENGTH: 7
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Best Local
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APPLICANT: GERRATY, No. US20020187925Alman L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
                                             APPLICANT:
                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22 NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
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CURRENT FILING DATE: 2001-01-12
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PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/0
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
                           APPLICANT:
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CURRENT FILING DATE: 2001-01-12
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OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
                    Sun, Ming
Hu, Weiming
                                                               Costello,
                                                                                                                                                     Application US/09997900
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Pred. No.
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/997,900 CURRENT FILING DATE: 2001-11-30

TITLE OF INVENTION: in Plants FILE REFERENCE: 043753/241148 (5849-20A)

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US-09-758-128-44

Sequence 44, Application US/09758128
Patent No. US20020107187A1
GENERAL INFORMATION:
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                                                                                       RESULT 8
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LOCATION: (1)..(2)

OTHER INFORMATION: Thrombin cleavage site
US-09-997-900-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/106,239
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 09/426,568
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEO ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 10
                                                                                                                                                                                                                 Best Loc
Matches
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Best Local Similarity 100
Matches 4; Conservative
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TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US/09/758,128

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR PILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-05-22

PRIOR FILING DATE: 1996-05-22
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APPLICANT: KINGSTON, David J.
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APPLICANT: GERRATY, No. US20020107187Alman L.
APPLICANT: WESTBROOK, Simon L.
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NAME/KEY: PEPTIDE
LOCATION: (1)..(7)
OTHER INFORMATION: N-terminal
OTHER INFORMATION: of plasmid
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TYPE: PRT
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nes 4; Conserv
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Pred. No. 1.1
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RESULT 9
US-09-309-196-96
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CURRENT APPLICATION NUMBER: US/09/758,128
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
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APPLICANT:
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                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                           APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 419 Seven
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
              NAME: COOPER, IVER P. REGISTRATION NUMBER: 28 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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TRUEHEART, JOSHUA
TRUEHEART, JOSHUA
VENTION: YEAST CELLS ENGINEERED TO PRODUCE
VENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BROACH, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLEIN, Christine
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Pred. No. 1.
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: 49 Human Secreted Proteins

FILE REFERENCE: P2032P1

CURRENT APPLICATION NUMBER: US/09/904,615

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 09/511,554

PRIOR APPLICATION NUMBER: 60/097,917

PRIOR APPLICATION NUMBER: 60/097,917

PRIOR FILING DATE: 1998-08-25
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US-09-904-615-118
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                                                                                                                                                                             Sequence 118, Application US/09904615
Patent No. US20020026040A1
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SEQ ID NO 118
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Best Local Similarity 100.
Matches 4; Conservative
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EARLIER FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 60/097,917
EARLIER FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 60/098,634
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NUMBER OF SEQ ID NOS: 170
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CURRENT FILING DATE: 2000-12-1
EARLIER APPLICATION NUMBER: 09
EARLIER FILING DATE: 2000-02-2
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TITLE OF INVENTION: 49 Human Secreted Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (19)
COTHER INFORMATION: Xaa equals stop translation
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TELEFAX: 202-7
TELEX: 248633
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Pred. No.
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Pred. No.
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Patent No. US20020048763A1
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LENGTH: 19
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PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver. 2.0
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PRIOR FILING DATE: 2000-09-27
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NAME/KEY: SITE
LOCATION: (19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SLDA 4
                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SLDA 4
                                                                      APPLICATION NUMBER: US 60/234,687
                                                                                                                        FILING DATE: 2001-0 APPLICATION NUMBER:
                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                     FILING DATE: 2000-06-30
                                    FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
                                                                                                    FILING DATE: 2001-01-30
                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 24263.6
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Chen, Wensheng
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Hanzel, David K.
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                                                                                                                                             2001-01-30
                                                                                                                                                                                    2001-01-30
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09/774,203
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Pred. No. 32;
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NUMBER OF SEQ ID NOS: 49117

SOPTWARE: Annomax Sequence List1

SEQ ID NO 45603

LENGTH: 34

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC013
OTHER INFORMATION: EXPRESSED IN
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US-09-864-761-35349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                     FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                           FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                              FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel, David K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Listing
                   2000-09-21
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IN FETAL LIVER, SIGNAL = 0.77
IN BRAIN, SIGNAL = 0.7
IN BONE MARROW, SIGNAL = 0.68
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Pred. No.
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; SEQ ID NO 54
; LENCTH: 45
; TYPE: PRT
; ORGANISM: Beetle
US-10-004-717-54
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US-10-004-717-54
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35349
                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   NUMBER OF SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE.

TITLE OF INVENTION: ATOMAL ASSOCIATED SEQUENCE FOR DEAFNESS,

TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION

FILE REFERENCE: PO1899US4

CURRENT APPLICATION NUMBER: US/10/004,717

CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 09/585,645

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR APPLICATION NUMBER: 60/137,060

PRIOR APPLICATION NUMBER: 60/137,060

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 1999-06-01

PRIOR FILING DATE: 1999-06-01

PRIOR FILING DATE: 1999-06-01

PRIOR FILING DATE: 1999-06-01
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26 SLDA
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R INFORMATION:
R INFORMATION:
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INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.1
                                                                                                100.0%; ilarity 100.0%; Conservative
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N. EXPRESSED IN BONE MARROW, SIGNAL = 1.3

N. EXPRESSED IN HELA, SIGNAL = 2.2

N. EXPRESSED IN HELA, SIGNAL = 2.2

N. EXPRESSED IN HELA, SIGNAL = 1.3

N. EXPRESSED IN HBL100, SIGNAL = 1.4

N. EXPRESSED IN LONG, SIGNAL = 1.6

N. EXPRESSED IN BRAIN, SIGNAL = 1.6

N. EXPRESSED IN BRAIN, SIGNAL = 1.7

N. EXPRESSED IN BRAIN, SIGNAL = 1.7
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Pred. No.
                                                                                                                        Score 18;
Pred. No.
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80;
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RESULT 15 US-09-729-674-68

Sequence 68, Application US/09729674 Patent No. US20010039335A1 GENERAL INFORMATION:

Jacobs, Kenneth McCoy, John M.

USEFUL

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Query Match
Best Local Similarity
----hes 4; Conserv
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                                                                                   ; NAME/KEY: UNSURE
; LOCATION: (46)
US-09-727-801-8
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US-09-727-801-8
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                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Allen, Steve
APPLICANT: Helentjaris, Tim
APPLICANT: Helentjaris, Tim
TITLE OF INVENTION: Homologs of SCF Ubiquitin-Ligase Complex Component
FILE REFERENCE: BB1418 US NA
CURRENT APPLICATION NUMBER: US/09/727,801
CURRENT FILING DATE: 2000-12-01
CURRENT FILING DATE: 2000-12-01
                                                                                                                                                                           SEQ ID NO 8
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US
Patent No. US20010034059A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver.
SEQ ID NO 68
LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-
                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: UNSURE LOCATION: (39)
NAME/KEY: UNSURE LOCATION: (45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 283
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
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SEQ ID NO 34730
LENGTH: 55
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR APPLICATION NUMBER: GB :
PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR EILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2001-01-30
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION:
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
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Chen, Wensheng
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DD IN BRAIN, SIGNAL = 1.7

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ED IN HBL100, SIGNAL = 2.1

ED IN HEART, SIGNAL = 2.1

ED IN LUNG, SIGNAL = 2

ED IN ADULT LIVER, SIGNAL = 1

ED IN FETAL LIVER, SIGNAL = 2

FI HIT: P09095, EVALUE 3.40e+
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US-09-74-887-267

; Sequence 267, Application US/09764887

; Patent No. US20020042096A1

; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-887-267
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US-10-001-876-181
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Best Local Similarity
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Matches 4
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SEQ ID NO 181
LENGTH: 58
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                                                                     Query Match
Best Local (
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PALI3
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and FILE REFERENCE: DEX-0285
CURRENT APPLICATION NUMBER: US/10/001,876
CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                    Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 658
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PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 211
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Cafferkey, Robert
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Pred. No. 1.1e+02;
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Pred. No.
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PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: B 24263.6

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
                                                   Query Match
Best Local S
Matches 4
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NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 46194

LENGTH: 62

TYPE: PRT
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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OTHER INFORMATION: EXPRESSED IN BRAIN
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OTHER INFORMATION: EXPRESSED IN ADJULT
OTHER INFORMATION: EXPRESSED IN FUTAL
OTHER INFORMATION: EXPRESSED IN FUTAL
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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                                                   Similarity 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel,
                                                100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                            EXPRESSED IN BRAIN, SIGNAL = 1.6

EXPRESSED IN PLACENTA, SIGNAL = 1.5

EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

EST_HUMAN HIT: AA868675.1, EVALUE 7.00e-31

SWISSPROT HIT: P08960, EVALUE 2.60e+00
                                                     0;
                                                                           Score 18; DB 10;
Pred. No. 1.1e+02;
                                                        Mismatches
                                                                                                   Length 62;
                                                        Indels
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                                                     Gaps
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RESULT 22
US-09-864-761-34065
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US-09-796-692-1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-796-692-1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; PRIOR FILING DATE: 2000
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for W
; SEQ ID NO 1225
; LENGTH: 64
; TYPE: PRT
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                           Sequence 34065, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
              APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                          APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
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                                                                                                                                                                                                                                                                                                                                                      42 SLDA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 4; Conserv
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APPLICATION NUMBER: 60/223,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/218,950 FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-05-01
APPLICATION NUMBER: 60/202,084
FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/200,545 FILING DATE: 2000-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/200,779
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  NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for Windows Version
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60/180,312
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Pred. No. 1.2e+02;
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                                                                                                   PROBES
                                                                                               USEFUL FOR
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US-08-424-550B-33
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US-09-864-761-34065
                                                                            Matches
                                                                                                             Query Match
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OTHER INFORMATION: 1
OTHER INFORMATION: 1
OTHER INFORMATION: 1
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PRIOR
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE: OTHER INFORMATION: MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
11
                                   1 SLDA 4
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APPLICATION NUMBER:
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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 SLDA 14
                                                                                             Similarity
                                                                            Conservative
                                                                                                                                                                                                                                        N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.

N: EXPRESSED IN HELA; SIGNAL = 0.77

N: EXPRESSED IN HELA; SIGNAL = 1.1

N: EXPRESSED IN HEART, SIGNAL = 1.8

N: EXPRESSED IN DIACENTA, SIGNAL = 3.8

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.4
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SWISSPROT
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                                                                                           100.0%;
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                                                                                                                                                               IN BONE MARROW, SIGNAL = 0.78
IN HBL100, SIGNAL = 1.4
HIT: BE746542.1, EVALUE 5.00e-35
HIT: Q15750, EVALUE 4.00e-36
                                                                          0;
                                                                                         Score 18; DB 10;
Pred. No. 1.3e+02;
                                                                Mismatches
                                                                                                             Length 70;
                                                                            Indels
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                                                                                                                                                                                                                                                                                    0.73
                                                                          0;
                                                                          Gaps
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Sequence 33, Application US/08424550B Patent No. US20020119447A1 GENERAL INFORMATION:

APPLICANT:

JOHN N.

SIMONS PILOT-MATIAS

SCHLAUDER

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RESULT 24
US-09-764-869-1073
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                                                                                                                                       Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1073
LENGTH: 77
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1073, Application US/09764869 Patent No. US20020061521A1
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
SOFTWARE: PATENTIN RELEASE #1.0, Vers
CURRENT APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
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APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BULJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-B. NON-C, NO
TITLE OF INVENTION: REAGENTS AND METHODS FO
NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
FEATURE:
NAME/KEY: SITE
LOCATION: (26)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100 nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 SLDA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ABBOTT PARK
STATE: IL
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100.0%; Pred. No. 1.
tive 0; Mismatches
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Qy
                                                                   ; NAME/KBY: SITE ; LOCATION: (28) ; COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-877-1348
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US-09-764-877-1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens US-09-925-300-1880
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US-09-925-300-1880
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                                                                                                                                                                      SOFTWARE: PatentIn v
SEQ ID NO 1348
LENGTH: 78
TYPE: PRT
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1880
LENGTH: 77
TYPE: PRT
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Best Local Similarity 100.0%;
Matches 4; Conservative
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                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                         Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890 SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 SLDA 70
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Local Similarity es 4; Conserv
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                100.0%; Score 18; 100.0%; Pred. No.
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Pred. No.
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Pred. No.
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                                 Length 78;
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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Annomax Seque
; SEQ ID NO 40746
; LENGTH: 79
; TYPE: PRT
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                                                                                                                                                                    OTHER INFORMATION:
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                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                 FEATURE:
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PRIOR FILING DATE: 2000-05-26
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: US 60/234,687
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D. US20020048763A1
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k, David R.
zel, David K.
N: MAP TO AL138796.2

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86

N: EXPRESSED IN BRAIN, SIGNAL = 0.86

N: EXPRESSED IN PLACENTA, SIGNAL = 0.64

N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.54

N: EXPRESSED IN BONE MARROW, SIGNAL = 0.55

N: EXPRESSED IN HEART, SIGNAL = 2.6

N: EXPRESSED IN HEART, SIGNAL = 2.6

N: EST_HUMAN HIT: H29179.1, EVALUE 2.00e-21

N: SWISSPROT HIT: P21179, EVALUE 3.30e+00
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RESULT 29
US-09-925-300-1597
; Sequence 1597, Application
; Patent No. US20020151681A1
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US-09-764-877-1555
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1597
LENGTH: 83
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APPLICANT: Rosen et al.
                                                                 CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
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                                                                                                                                        APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                        PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                  APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC005
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (72)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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Pred. No. 1.5
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: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-300-1597
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US-10-108-605-281
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                                      ; ORGANISM: Drosophila melanogaster US-10-108-605-281
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 85
TYPE: PRT
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APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
TITLE OF INCENTION: MAMMALIAN SECRETED PROTEINS
                                                                                          PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 281
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 281, Application US/10108605 Patent No. US20020160934A1
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                         APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 00-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 100.0%;
Local Similarity 100.0%;
hes 4; Conservative 0
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  100.0%;
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  Score 18;
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thes 0;
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  DΒ
  9;
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; ORGANISM: Homo sapiens
US-09-931-071-11
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US-09-931-071-11
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Patent No. US20020142979A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-330001
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Best Local S
Matches 4
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APPLICANT: Bertin, John
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-335001
CURRENT APPLICATION NUMBER: US/09/931,071
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/428,252
PRIOR FILING DATE: 1999-10-27
                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11
LENGTH: 89
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Matches 4; Conserv
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                                                                 Matches
                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/728,721
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/340,620
PRIOR FILING DATE: 1999-06-28
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/841,879B CURRENT FILING DATE: 2001-04-24
                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                      LENGTH: 90
TYPE: PRT
                                                                                 Local Similarity
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25 SLDA 28
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Pred. No.
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RESULT 34 US-10-002-974-21 ; Sequence 21, Ap

Application US/10002974

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CURRENT APPLICATION NUMBER: US/10/002,974
CURRENT FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 92
TYPE: PAT
ORGANISM: Homo sapiens
US-10-002-974-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Ogur, Yasunori
TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
FILE REFERENCE: UM-06645
CURRENT APPLICATION NUMBER: US/10/014,269
CURRENT FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
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Best Local S
Matches 4
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells:
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 92
TYPE: PRT
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Local Similarity 100.0%;
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Cho, Judy
Nicolae, Dan L
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Pred. No. 1.7e+02;
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Pred. No. 1
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RESULT 38
US-09-905-243-49
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LOCATION: (50)...(66)

; OTHER INFORMATION: CDRII

US-09-905-243-48
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US-09-905-243-48
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Best Local Similarity
"~+~hes 4; Conserv:
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GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905, 243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
                                                                                                                                                                                                                                                                                       Sequence 49, Application US/09905243
Patent No. US20020062009A1
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 48

LENGTH: 98

TYPE: PRT

ORGANISM: Macaca cynomolgus
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PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 338
LENGTH: 96
THEORY IN THE PRIOR OF THE PRIOR O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Monoclonal Antibodies with Reduced TITLE OF INVENTION: Immunogenicity FILE REFERENCE: P50770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/300,970 PRIOR FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Taylor, Alexander H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (31)...(35)
OTHER INFORMATION: CDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: DOMAIN
LOCATION: (31)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 SLDA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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Pred. No. 1
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Pred No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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1.9e+02;
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US-09-939-980-515; Sequence 515, A
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SOFTMARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 49
LENCTH: 98
TYPE: PRT
ORGANISM: Macaca cynomolgus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. US20020082234A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-04-28 NUMBER OF SEQ ID NOS: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: DOMAIN
LOCATION: (31)...(35)
OTHER INFORMATION: CDRI
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                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ward, Judith
TITLE OF INVENTION: NO. US20020082234Alel Prokaryotic Polynucleotides,
NUMBER OF SEQUENCES: 534
CORRESONECE ADDRESS:
                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPRATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 510-270-4478
                                                                                                                                                           APPLICATION NUMBER: 08/936,165 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                        NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                   TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09939980
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CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Knowles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hodgson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   onetto, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Pred. No. 1.9e+02;
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TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 515:
US-09-939-980-515
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SOFTWARE: Fas
SEQ ID NO 231
LENGTH: 109
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT: Bertin, John
                                                                                                                                                                                                                                                                                                                    Sequence 231, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
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Best Local
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Best Local Similarity
                                                                            FILE REFERENCE: 00786/361003
CURRENT APPLICATION NUMBER: US/09/975,719
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/199,637
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: US 60/066,517
PRIOR FILING DATE: 1997-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR ETILING DATE: 199-02-05
PRIOR RIPLICATION NUMBER: EARLIER FILING DATE: 1999-02-05
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR ETILING DATE: EARLIER FILING DATE: 1998-06-17
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
PRIOR: FILING DATE: EARLIER FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 07334/118001
                                                                                                                                                                                                                     TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/118,984
CURRENT FILING DATE: 2002-04-09
                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                            APPLICANT: Ausubel, Frederick M. APPLICANT: Rahme, Laurence G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           28 SLDA 31
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nes 4; Conserv
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                                         FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10118984 No. US20020197693A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                    Application US/09975719 o. US20030022349A1
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ilarity 100.0%;
Conservative 0
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                                           Windows Version 4.0
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Pred. No. 2e+02;
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US-10-105-931-6
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US-09-728-721-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR PAPLICATION NUMBER: 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa US-09-975-719-231
                                                                                                                                           NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10105931
Patent No. US20020150987A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
                                                                               LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
-10-105-931-6
             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/105,931
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09728721 Patent No. US20020061845A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-076001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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CURRENT FILING DATE: 2000-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001
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les 4; Conserv
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         Similarity 4; Conserv
   100.0%; Score 18; DB 12; ilarity 100.0%; Pred. No. 2.1e+02; Conservative 0; Mismatches 0;
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Pred. No. 2.1e+02;
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Pred. No. 2.1e+02;
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                                     Length 109;
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Search completed: February Job time: 6.83333 secs
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; TYPE: PAT
; ORGANISM: Toxoplasma gondii
US-09-216-393-58
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US-09-216-393-58
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Best Local
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leach,
APPLICANT: Mehrab
APPLICANT: Conley
APPLICANT: Law, D
APPLICANT: Topper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1788, Application US/09867550 Patent No. US20020082206A1 GENERAL INFORMATION:
                                                                                                                                                Matches
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CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58, Application US/09216393
Patent No. US20010014447A1
GEMERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: TX-1-C2
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206 lel Polynucleotides from Atherogenic Cells a
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313) |
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US81 60/208/427
PRIOR APPLICATION NUMBER: US8N 60/208/427
PRIOR FILING DATE: 2000-05-30
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Best Local Similarity
                                                                                                                                                                                                                                                       LENGTH: 118
TYPE: PRT
                                                                       110 SLDA 113
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                                                                                                                                          Local Similarity nes 4; Conserv
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Conley, Pamela
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              2003, 11:39:45
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Pred. No. 2.3e+02;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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2: /cgn2_6/ptodata/1/paa/US

3: /cgn2_6/ptodata/1/paa/US

4: /cgn2_6/ptodata/1/paa/US

5: /cgn2_6/ptodata/1/paa/US

6: /cgn2_6/ptodata/1/paa/US

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19.366 Million cell updates/sec
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/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
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US-09-194-218-44
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                                                Sequence 45, Appl
Sequence 48, Appl
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	sequence 15,	n (16 2001	, <u>-</u>	ര	е 96,	equence 32,	e 32,	96,	e 96,	e 32,	e 32,	96,	96,	e ω	2, Ap	e 13,	13, Ap	647	271,	12	25,	12, App	e 12,	quence 12, Appl	equence 10, App	44, App	•	44, App	41,	4	41,	44,	e 41,	e 53,	e 53,	υ U	Sequence 53, Appl

ALIGNMENTS

US-08-981-824-45

US-08-981-824-45

Sequence 45, Application US/08981824

GENERAL INFORMATION:

APPLICANT: ENDL, Josef

APPLICANT: SCHENDEL, Dolores

APPLICANT: ALBERT, Winfried

APPLICANT: SCHENDEL, Dolores

APPLICANT: VAN ENDERT, Peter

APPLICANT: VAN ENDERT, Peter

APPLICANT: USOFTAND, Christian

APPLICANT: JUNG, Gunther-Gerhard

TITLE OF INVENTION: AUTOREACTIVE PEPTIDES FROM HUMAN GLUTAMIC ACID

TITLE OF INVENTION: DECARBOXYLASE (GAD)

FILE REFERENCE: 564-7029

CURRENT APPLICATION NUMBER: US/08/981,824

CURRENT FILING DATE: 1998-09-18

EARLIER APPLICATION NUMBER: PCT/EP96/03093

EARLIER APPLICATION NUMBER: PCT/EP96/03093

EARLIER APPLICATION NUMBER: DE/195 25 784.7

EARLIER FILING DATE: 1995-07-14

NUMBER OF SEQ ID NOS: 47

SOFTMARE: Patentin Ver. 2.1

SEQ ID NO 45

LENGTH: 6

TYPE: PRT

ORGANISM: Homo sapiens

US-08-981-824-45

Ouery Match

100.0%; Score 18; DB 13; Length 6;

Best Local Similarity

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RESULT 3
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                                                                                                                                 Sequence 48, Application US/08462860
GENERAL INFORMATION:
APPLICANT: Barry S. Cooperman, Ha
APPLICANT: Jerome Salem, and Alis
                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: The University of Pennsylvania
TITLE OF INVENTION: "Plasmodium falciparum Ribonucleotide Reductase, DNA
TITLE OF INVENTION: Sequences Therefor and Peptide inhibitors Thereof"
NUMBER OF SEQUENCES: 67
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SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9
FILING DATE: NOT YET ASSIGN
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: None
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavorg
STREET: Two Penn Center Plaza
STREET: Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                              APPLICANT: Barry S. Cooperman, Harvey Rubin,
APPLICANT: Jerome Salem, and Alison L. Fisher
TITLE OF INVENTION: "Peptide Inhibitors of
TITLE OF INVENTION: plasmodium Falciparum Ribonucleotide Reductase"
NUMBER OF SEQUENCES: 67
                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGIASTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 39:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/13
FILING DATE: 14 October 1
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: IBM PS/2
     STREET:
CITY: I
                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Monaco, Daniel REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                     2 SLDA 5
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                                                                                                                                                                                                                                                                                                                                                     h 100.0%; Score 18; DB 1; Similarity 100.0%; Pred. No. 4.2e+0(4); Conservative 0; Mismatches
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19103
         3: Seidel, Gonda, Lavorgna & Monaco, P.C.
Suite 1800, Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/136,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT/US94/11416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48:
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                                                                                                                                                                                                                                                                                                                                                                        .2e+06;
                                                                                                                                                                                                                                                                                                                                                                                        Length 7;
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US-08-462-860A-48
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                                                                                                                                      COUNTY...
ZIP: 19102-1/60
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOMPUTER: IBM PC COMPATIBLE
TOMPUTER: TOMPUTER: PC-DOS/MS-DOS'
TOMPUTER: TOMPUTER: PC-DOS/MS-DOS'
TOMPUTER: TOMPUTER: PC-DOS/MS-DOS'
TOMPUTER: PC-DOS/MS-DOS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/08462860A GENERAL INFORMATION:
APPLICATION NUMBER: US/08/462,860A FILING DATE: 05-JUN-1995 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/136,743 FILING DATE: 14-OCT-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cooperman, Barry S.
APPLICANT: Rubin, Harvey
APPLICANT: Salem, Jerome
APPLICANT: Fisher, Alison L.
TITLE OF INVENTION: RIBONUCLEO
TITLE OF INVENTION: REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-883
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: October
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                       CITY: Philadelphia
                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MONACO, DANIEL A.
MONACO, DANIEL A.
30,480
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Suite 1800,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cooperman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE INHIBITORS OF PLASMODIUM FALCIPARUM
                                                                                                                                                                                                                                                                                                                                                                            REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                           RIBONUCLEOTIDE
                                                                                                                                                                                                                                                                                                     GONDA, LAVORGNA & MONACO, P.C., Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 18; DB 8; 100.0%; Pred. No. 4.2e+06;
                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                            US/08/462,860A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/136,743 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3957-10 DI1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
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3957-10 DI1

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US-09-194-218-44
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US-09-194-218-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-08-462-860A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-194-218-41
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                                                                                                                                                                                                                                                                  Sequence 44, Application US/09194218 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/09194218 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
          TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: US/09/194,218

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: PCT/AU97/00312

EARLIER FILING DATE: 1997-05-22

EARLIER FILING DATE: 1997-05-22

EARLIER FILING DATE: 1996-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/194,218
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: PCT/AU97/00312
EARLIER FILING DATE: 1997-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KINGSTON, David J. APPLICANT: GERRATY, Norman L. APPLICANT: WESTBROOK, Simon L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                     APPLICANT: KINGSTON, David J. APPLICANT: GERRATY, Norman L. APPLICANT: WESTBROOK, Simon L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: AU PN9990
EARLIER FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watch 100.0%; Score 18; DB 15; Local Similarity 100.0%; Pred. No. 4.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 amino acids
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Pred. No. 4.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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US-09-194-218-44
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                                                                                                              US-09-396-347D-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-396-347B-53
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                                                                                                                          SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 53

LENGTH: 7

TYPE: PRT

ORGANISM: Mycobacterium tuberculosis strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/396,347B
CURRENT EILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Thes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 44
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53, Application US/09396347B GENERAL INFORMATION:
                                               Matches
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/09396347D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                       CURRENT FILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                      APPLICANT: Laal, Suman
APPLICANT: Zolla-Pazner, Susan
APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: 32004-169276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: NYU-11/CIP
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APPLICANT: Zolla-Pazn
APPLICANT: Belisle, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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100.0%; Pred. No. 4.2e+06;
live 0; Mismatches 0;
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                                                          Score 18; DB 17;
Pred. No. 4.2e+06;
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Pred. No. 4.2e+06;
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RESULT 11
US-09-758-128-41
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Sequence 41, Application US/09758128
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, Norman L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-396-347F-53
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; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-396-347E-53

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SEQ ID NO 53
LENGTH: 7
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APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: 32004-169276
CURRENT APPLICATION NUMBER: US/09/396,347F
CURRENT FILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 106
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Best Local Similarity
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CURRENT FILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 106
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APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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Pred. No. 4.2e+06;
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US-09-758-128-44
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                                                                                                                                                                                                                                                                          Sequence 41, Applica GENERAL INFORMATION:
                                                                                                                                    APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, Norman L.
APPLICANT: GERRATY, Norman L.
APPLICANT: WESTBROOK, SIMON L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
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SEQ ID NO 44
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CURRENT APPLICATION NUMBER: US/09/758/198

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
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CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
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APPLICANT: GERRATY, NORMAN L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
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Best Local
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PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
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NUMBER OF SEQ ID NOS: 58
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CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
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Similarity 100.0%;
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Pred. No. 4.2e+06;
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Pred. No.
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hes 0;
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APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, NOTMAN L.
APPLICANT: GERRATY, NOTMAN L.
APPLICANT: GERRATY, NOTMAN L.
APPLICANT: GERRATY, NOTMAN L.
APPLICANT: MESTBROOK, SIMON L.
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,198
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: DATE: DATE: 1997-05-22
PRIOR APPLICATION ONMER FILING DATE: 1996-05-22
PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
COUNTAINED ON THE PRIOR FILING DATE: 1996-05-22
NUMBER: DATE: EARLIER FILING DATE: 1996-05-22
FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41
LENGTH: 7
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US-09-758-198-44
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US-09-758-426-41
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US-09-758-198-44
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                                                                                                                                                                                                                                                    Sequence 41, Application US/09758426
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, Norman L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AN
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TYPE: PRT
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nilarity 100.0%;
Conservative 0;
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Pred. No. 4.2e+06;
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Best Local Similarity
"hes 4; Conserv?
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; ORGANISM: Rat
US-09-758-426-44
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                                                                                  ; ORGANISM: Homo sapiens US-09-861-661-41
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-861-661-41; Sequence 41, Application US/09861661; GENERAL INFORMATION:
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LENGTH: 7
                                                                                                                                                                SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 44, Application US/09758426
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, NOTMAN L.
APPLICANT: WESTBROOK, SIMON L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
CURRENT FILING DATE: 016786/0214
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: AU PN9990
DEBICE TITLE DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
  Query Match 100
Best Local Similarity 100
Matches 4; Conservative
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                                                                                                                                                                              PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                        APPLICANT: WESTBROOK, SIMON L. TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF FILE REFERENCE: 054270/0135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/194,218 PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/861,661
CURRENT FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KINGSTON, DAVID J. APPLICANT: GERRATY, NORMAN L.
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: AU PN9990
                                                                                                                                         LENGTH:
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100.0%; Score 18; DB 22; 100.0%; Pred. No. 4.2e+06; O: Mismatches 0;
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Pred. No. 4.2e+06;
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US-09-997-900-10
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Best Local S
Matches 4
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GENERAL INFORMATION:
APPLICANT: KINGSTON, DAVID J.
                                                                                                                                                                                                                                                                                                                               SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09997900 GENERAL INFORMATION:
                       Query Match
Best Local :
      Matches
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TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
TITLE OF INVENTION: in plants
FILE REFERENCE: 043753/241148 (5849-20A)
CURRENT APPLICATION NUMBER: US/09/997,900
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/106,239
PRIOR APPLICATION NUMBER: 60/106,239
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: AU PN9990 PRIOR FILING DATE: 1996-05-22 NUMBER OF SEQ ID NOS: 59
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CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
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APPLICANT: WESTBROOK, SIMON L.

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
FILE REFERENCE: 054270/0135
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/426,568 PRIOR FILING DATE: 1999-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kakefuda, Genichi
APPLICANT: Costello, Colleen
                                                                                                                                                                                                                                                     LENGTH: 7
TYPE: PRT
ORGANISM: Arabidopsis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7
TYPE: PRT
ORGANISM: Rattus sp.
                                                                                                 NAME/KEY: SITE LOCATION: (1)..(2) OTHER INFORMATION:
                                                                                                                                                        NAME/KEY: PEPTIDE
LOCATION: (1)..(7)
OTHER INFORMATION: N-terminal sequence
OTHER INFORMATION: of plasmid F2
                                                                                                                                                                                                                                                   FEATURE:
                     Local
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nes 4; Conserv
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  Similarity
4; Conserv
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100.0%; Score 18; DB 23; llarity 100.0%; Pred. No. 4.2e+06; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 18; DB 22; llarity 100.0%; Pred. No. 4.2e+06; Conservative 0; Mismatches 0;
                                                                                                 Thrombin cleavage site
                                                                                                                                                                                 of AHAS small subunit peptide
                                        Length 7;
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Gaps
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US-08-526-708-12
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                                                                                                                                                                                                                                                                                                             RESULT 21
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                                                                                                                                                                                                                                                                                          US-08-813-273-12
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COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/526,708
FILING DATE: 11-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathern
                                                                                                                                                                                                                                                     Sequence 12, Application US/08813273 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Applicat GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                             APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
TITLE OF INVENTION: Home to a Selected Organ or Tissue In
NUMBER OF SEQUENCES: 26
                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: both
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APPLICANT: Pasqualini, Rena
                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 100.0%;
Local Similarity 100.0%;
hes 4; Conservative 0;
                                                                         STATE:
                                                                                         CITY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 92122
                                       ZIP: 92122
                                                        COUNTRY:
                                                                                                          STREET:
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                                                    California
C: United States
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: United States
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                                                                                                        E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
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Floppy disk
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Pred. No. 4.2e+06;
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US-09-228-866-12
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9049
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09228866 GENERAL INFORMATION:
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                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/526,708
APPLICATION NUMBER: US 08/526,708
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.5
REFERENCE,/DOCKET NUMBER: P-LJ 3430
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
FENCION
TOPOLOGY: bo:
MOLECULE TYPE:
9-228-866-12
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,273
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules That Home to a Selected Organ
TITLE OF INVENTION: In Vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/228,866 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 8 amino acids
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                                  amino acid
GY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                         8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruoslahti, Erkki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 12; 100.0%; Pred. No. 4.2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
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RESULT 24
US-09-922-227-12
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; TYPE: PRT
; ORGANISM: Mucor hiemalis
US-09-700-993-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us-09-700-993-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09922227
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
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Best Local Similarity 100.
Matches 4; Conservative
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CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: JP98/141717
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KOBAYASHI, KAZUO
APPLICANT: TAKEUCHI, MAKOTO
APPLICANT: IWAMATSU, AKIHIKO
APPLICANT: YAMAMOTO, KENJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ENDO-BETA-N-ACETYLGLUCOSAMINIDASE GENE FILE REFERENCE: 081356/0154
                                                          ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/922,227

FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                        Pasqualini, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
Home to a Selected Organ In Vivo
                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                           ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
           APPLICATION NUMBER: US 08/526,710 FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                               STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUMAGAI, HIDEHIKO
YOSHIDA, SATOSHI
                                                                                                                                                                                                                                                            COUNTRY: United States
APPLICATION NUMBER: US 08/813,273
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Pred. No. 4.2e+06;
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RESULT 26
US-10-014-340-647
; Sequence 647, Application US/10014340
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: homo sapien US-09-988-493-271
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MOLECULE TYPE: peptide;

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-922-227-12
                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                          Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 271
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/GB01/01219
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: GB 0006695.1
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: GB 0007265.2
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri APPLICANT: O'Hare, Michael John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/988,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Waterfield, Michael Derek
TITLE OF INVENTION: Proteins, Genes, and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
FILE REFERENCE: 2543-1-024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICATION NUMBER: US 09/227,906
FILING DATE: 08-JAN-1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page, Martin John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/862,855 FILING DATE: 23-MAY-1997
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                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                        100.0%;
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619) 535-8949
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100.0%; P
tive 0;
                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                      Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 23;
Pred. No. 4.2e+06;
; Mismatches 0;
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                    4.2e+06;
                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                   Length 8;
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RESULT 28
US-09-109-836-13
; Sequence 13, Application US/09109836
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                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 647
LENGTH: 8
TYPE: PRT
                                                                                                                                                                        Query Match
                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US97/21437
FILING DATE: 26-NOV-1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/031,607
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 9195-078
CURRENT APPLICATION NUMBER: US/10/014,340
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                            TELEFAX: 617-
TELEX: 200154
                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & ALL. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                             1 SLDA 4
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                                                                                 SLDA 10
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                                                                                                                                             Conservative
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                                                                                                                                                        100.0%;
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                                                                                                                                           0;
                                                                                                                                          Score 18; DB Pred. No. 4.8 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        00786/360WO2
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                                                                                                                                                          4.8e+02;
                                                                                                                                                                     Length 10;
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                                                                                                                                          Indels
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                                                                                                                                       Gaps
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RESULT 29
US-08-188-354-2
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                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08188354
GENERAL INFORMATION:
APPLICANT: COMAN, Nicholas J.
TITLE OF INVENTION: NOVEL EUKARYOTIC FOLDING PROTEINS, NUCLEIC
TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF MAKING AND USING THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 02-JUL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/977,836
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 60/031,607
FILING DATE: 27-NOV-1996
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,354
                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: FC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jacobowitz Israel, Esther APPLICANT: Simister, Neil E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELLEFAX: or.
TELEFAX: 200154
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                                                                                                                                                                             STREET: *1.
CITY: Washington
                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 18; DB 15; Local Similarity 100.0%; Pred. No. 4.8e+02; ses 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225 |
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish a .....
cmpreT: 225 Franklin Street
                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                               20004
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02110-2804
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                                                                                                                                                                                                                  419 Seventh Street, N.W., Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                   BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
28-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODULATION OF IGG BINDING TO FCRN
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                                            US-08-461-383-96
                                                              RESULT 31
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US-09-831-253A-3
           ; Sequence 96, Applicat; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: EZQUERCO SAENZ, Ignacio Jose
APPLICANT: LASARTE SAGASTIBELZA, Juan Jose
APPLICANT: PRIETO VALTUENA, Jesus
APPLICANT: BORRAS CUESTA, Francisco
TITLE OF INVENTION: TGF(b1-inhibitor peptides
FILE REFERENCE: U013446-9
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 3
LENGTH: 12
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Matches 4; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/I
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/897,162
APPLICATION NUMBER: US 07/897,162
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                     Local Similarity
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TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
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                                                                                                                                       1 SLDA 4
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                               Application US/08461383
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FOWLKES, Dana M.
                                                                                                                                                                        Conservative
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                                                                                                                                                                                    100.0%;
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APPLICANT:

BROACH, Jim MANFREDI, John KLEIN, Christine

APPLICANT:

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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                               Sequence 96, Application US/08463181 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                TITLE OF INVENTION:
                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR NUMBER OF SEQUENCES: 119
CORRESPONDE ADDRESS: ADDRESS:
                                                                                                                                                APPLICANT:
                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                APPLICANT:
                                                                                APPLICANT:
                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: CPI-012CP4B TELECOMMUNICATION INFORMATION: TELEPHONE: 617-227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-007-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0: FILING DATE: 31-JAN-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/041,431 FILING DATE: 31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 05-JUI
                                                                                                                                                                                                                                                                                                               1 SLDA 4
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               SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 amino acids
PAUL, Jeremy
TRUEHEART, Joshua
VENTION: YEAST CELLS ENGINEERED TO PRODUCE
VENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
EQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617-227-5941
                                                                                                                                             BROACH, Jim
                                                                                                              KLEIN, Christine
                                                                                                                          MANFREDI, John
                                                                                             MURPHY, Andrew J.
                                                                                                                                                           FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MURPHY, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                            100.0%; ; 100.0%; ; itive 0;
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                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 8;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                       Length 13;
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                         AND USES THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-463-181-96
                                                                                                                                                                                          Sequence 32, Application US/08689172A GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Co
TITLE OF INVENTION: Identifying Re
NUMBER OF SEQUENCES: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/041,431 FILING DATE: 31-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                          STREET: 60 St
CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELLEFAX: 202
TELEFAX: 248633
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W!,
                                                                                                                      ADDRESSEE: LAHIVE & CURRENTED STREET: 60 State Street, suite 510
                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202 - TELEPHONE: 202-737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08 FILING DATE: 13-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 05-JUJ CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                    5 SLDA
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                                                                        02109-1875
                                                                                                          Massachusetts
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                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 8;
Pred. No. 6.5e+02;
Mismatches 0;
                                                                                                                                                                                                          Receptor Effectors
                                                                                                                                                                                                                          Compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13;
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; MOLECULE TYPE:
US-08-689-172C-32
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GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Identifying Receptor Effectors
NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-9941
INFORMATION FOR SEQ ID NO: 32:
 Query Match 100.0%; Score 18; I Best Local Similarity 100.0%; Pred. No. 6. Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/689,172C
FILING DATE: 07-Aug-1996
CLASSIFICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REGISTRATION NUMBER: CPI-012CP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                      TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
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LENGTH: 13 amino acids
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 18; DB 10; Local Similarity 100.0%; Pred. No. 6.5e+02; les 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07 CLASSIFICATION:
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                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                   LENGTH:
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                                                                                                                             amino acid
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                                                                                          protein
   Mismatches
                                         DB 10;
                     .5e+02;
                                     Length 13;
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                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1002
ATTODNICY /*----
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-227-7400
TELEFAX: 617-227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08
FILING DATE: 05-UNN-1995
APPLICATION NUMBER: US 08
FILING DATE: 13-CCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/461,383
APPLICATION NUMBER: US 08/461,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: LAHIVE AND COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: CPI-012CP4B
                                                                                                                                                                                                                                                                                                                                                                               NAME: Vincent, Matthew P REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                          TOPOLOGY:
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                                     1 SLDA 4
5 SLDA 8
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                                                                        100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOWLKES, Dana M.
                                                                                                                                                                  peptide
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20-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 08/322,137
                                                                          0;
                                                                        Score 18; DB 16;
Pred. No. 6.5e+02;
; Mismatches 0;
                                                                                                          Length 13;
                                                                          Indels
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0,

Gaps

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SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-309-196-96
                                                                                                RESULT 37
US-09-747-774A-32
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                                                             Sequence 32, Application US/09747774A GENERAL INFORMATION:
                                                                                                                                                                                                                                     Query Match 100.0%; 9
Best Local Similarity 100.0%; 1
Matches 4; Conservative 0;
                           APPLICANT: Klein, Christine A. APPLICANT: Murphy, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGE...
ATTORNEY AGE...
ATTORNEY AGE...
NAME: COOPER, 1v...
REGISTRATION NUMBER: Zo,
REFERENCE/DOCKET NUMBER: FOLM..
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-628-5197
TELECHONE: 202-633
TO NO: 96:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 96, Application US/09309196 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/
FILING DATE: 31-TAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PAUL, Jeremy
APPLICANT: TRUEHBART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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                                                                                                                                                                                                          1 SLDA 4
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          Murphy, Andrew J. M. Broach, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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KLEIN, Christine
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                                                                                                                                                                                                                                                    Score 18; DB 17;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                  Length 13;
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US-09-953-354-32
; Sequence 32, Application US/09953354
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 18; DB 21; Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/461,383
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/463,181
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/322,137
PRIOR FILING DATE: 1994-10-13
PRIOR EPILING DATE: 1994-10-13
PRIOR EPILING DATE: 1994-10-13
PRIOR EPILING DATE: 1994-10-13
PRIOR EPILING DATE: 1994-10-13
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1994-01-31
PRIOR APPLICATION NUMBER: US 08/041,431
PRIOR FILING DATE: 1993-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1994-09-20 PRIOR APPLICATION NUMBER: US 08/190,328
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PRIOR APPLICATION NUMBER: US 08/461,598
PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/582,333
PRIOR FILING DATE: 1996-01-17
PRIOR APPLICATION NUMBER: US 08/464,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/747,774A CURRENT FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trueheart, Joshua
TITLE OF INVENTION: Methods and Compositions for Identifying
TITLE OF INVENTION: Receptor Effectors
FILE REFERENCE: CPI-012CP5DV
                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION UMBER: US/09/953,354
FILING DATE: 13-Sep-2001
CLASSIFICATION: Junknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 SLDA 8
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/689,172
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rlein, Christine A. APPLICANT: Rlein, Christine A. Murphy, Andrew J. M. Murphy, Andrew J. M. TITLE OF INVENTION: Methods and Compositions for Identifying Receptor Effectors
                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fowlkes, Dana M.
Trueheart, Joshu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAHIVE & COCKFIELD
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RESULT 39
US-10-263-341-96
Sequence 96, Application US/10263341
GENERAL INFORMATION:
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Best Local :
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TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32:
                 INFORMATION FOR SEQ ID NO: 96:
                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/322,137

FILING DATE: 13-OCT-1994

APPLICATION NUMBER: US 08/309,313

FILING DATE: 20-SEP-1994

APPLICATION NUMBER: US 08/190,328

FILING DATE: 31-JAN-1994

APPLICATION NUMBER: US 08/041,431

FILING DATE: 31-MAR-1993
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAUL, Jeremy
TRUEHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
SEQUENCE
                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/263,341 FILING DATE: 01-Oct-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                            TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                    NAME: COOPER, IVER P. REGISTRATION NUMBER: 28,005 REFERENCE/DOCKET NUMBER: FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOWLKES, Dana M. BROACH, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MURPHY, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MANFREDI, John
KLEIN, Christine
                                        248633
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                                                                                                                           FOLWKES=2C
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TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-10-263-341-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Derived from OTHER INFORMATION: the modified human type III receptor, position OTHER INFORMATION: 729-742 US-09-831-253A-6
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US-09-831-253A-6
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                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08400306 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PRIETO VALTUENA, Jesus
APPLICANT: BORRAS CUESTA, Francisco
TITLE OF INVENTION: TGF(b1-1nh1bitor
FILE REFERENCE: U013446-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: EZQUERRO SAENZ, Ignacio Jose APPLICANT: LASARTE SAGASTIBELZA, Juan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  APPLICANT: J.A. Kessler, A.J. Conley, B.A. Arnold
TITLE OF INVENTION: Selected Principal Neutralization
TITLE OF INVENTION: Epitopes for Antibody that Neutralizes HIV in Peripheral
TITLE OF INVENTION: Blood Mononouclear Cells
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                        STREET: P.O.
CITY: Rahway
STATE: NJ
             APPLICATION NUMBER: FILING DATE:
                                                                                                                                            ZIP: 07065
                                                                                                                                                       COUNTRY:
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5 SLDA 8
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CLASSIFICATION: 424
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                                                                                                                                                                                                         P.O. Box 2000
                                                                                                                                                          USA
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                                                                                                                                                                                                                   Co., Inc.
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                               US/08/400,306
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 22
Pred. No. 7e+02;
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RESULT 43
US-09-461-061-15
; Sequence 15, Application US/09461061
; GENERAL INFORMATION:
APPLICANT: MCCTRE, Keith R.
; TITLE OF INVENTION: Inhibition of Angiogenesis By High Molecular Weight
; TITLE OF INVENTION: Kininogen Domain 3 Peptide Analogs
: FILE REFERENCE: 6056-260 US
: FILE TITLE OF INVENTION NUMBER: US/09/461,061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Inhibition of Angiogenesis By High Moi TITLE OF INVENTION: Kininogen Domain 3 Peptide Analogs FILE REFERENCE: 6056-260 PC CURRENT APPLICATION NUMBER: PCT/US99/28465A CURRENT FILLING DATE: 1999-12-02 EARLIER APPLICATION NUMBER: 60/112/427 EARLIER FILLING DATE: 1999-12-16 SOFTWARE: PATENTIAL DATE: 1998-12-16 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 15 SEQ ID NO 1
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; OTHER INFORMATION: human HK domain 3
PCT-US99-28465-15
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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ANTI-SENSE: 1
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REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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LENGTH: 15 amino acids
TYPE: amino acid
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Local Similarity 100.0%;
les 4; Conservative 0
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PCT-US02-09671-65
; Sequence 65, Application PC/TUS0209671
; GENERAL INFORMATION:
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         PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-461-061A-15
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US-09-461-061-15
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EARLIER APPLICATION NUMBER: 60/11;
EARLIER FILING DATE: 1998-12-16;
NUMBER OF SEQ ID NOS: 21;
SOPTWARE: Patentin Ver. 2.0;
SEQ ID NO 15;
FENCING 16
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LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: MCCrae, Keith R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
                                                                                                                                                                                                TITLE OF INVENTION: TRANSLATIONAL PROFILING FILE REFERENCE: 08191-026W01
                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Inhibition of Angiogenesis By High Molecular Weight TITLE OF INVENTION: Kininogen Domain, 3 Peptide Analogs

CURRENT APPLICATION NUMBER: US/09/461,061A

CURRENT FILING DATE: 1999-12-15

PRIOR APPLICATION NUMBER: 60/112,427 |
PRIOR APPLICATION NUMBER: 60/112,427 |
PRIOR APPLICATION NUMBER: 60/112,427 |
PRIOR PILING DATE: 1998-12-16

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                          APPLICANT: Zycos Inc.
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ORGANISM: Artificial Sequence
FEATURE:
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NUMBER:
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Pred. No.
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PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09671-65
Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps O;
Search completed: February 6, 2003, 11:37:34
Job time: 134.167 secs
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    of hits satisfying chosen parameters:
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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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US-10-203-138A-12434
US-10-203-138A-12434
US-09-585-6458-54
PCT-US02-32727-24214
US-10-057-498-2975
PCT-US02-32727-17389
US-10-057-498-1775
PCT-US02-32727-2538
PCT-US02-32727-2713
US-10-057-498-2538
US-10-057-498-2538
US-10-057-498-27575
US-10-057-498-281948
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US-09-258-600-96 :
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; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,600
FILING DATE: 26-Peb-1999
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
UNIVERSELY OF THE PROPERTY OF THE PR
              ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOLW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FOWLKES, Dana M. BROACH, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
                                                                                                                                              APPLICATION NUMBER: US/08/461,598
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-OCT-1994
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
APPLICATION NUMBER: US 08/190,328
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: US 08/041,431
FILING DATE: 31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Seventh Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09258600
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PHEROMONE SYSTEM PROTEIN SURROGATE
F SEQUENCES: 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MANFREDI, John
  248633
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Seventh Street, N.W.,
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US-09/513
PCT-US02-32727-6416
US-10-057-498-6416
PCT-US02-32727-8518
US-10-057-498-8518
PCT-US02-32727-2064
PCT-US02-32727-6955
PCT-US02-32727-6955
PCT-US02-32727-69376
US-10-057-498-20376
US-10-057-498-23376
US-10-057-498-23376
US-10-057-498-23376
US-10-203-138A-11100
PCT-US02-32727-13114
PCT-US02-32727-77093
US-10-057-498-13114
US-10-057-498-13114
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RESULT 3
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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (25.5.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
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US-10-203-138A-12434
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                                                                                                                                                            Matches
                                                                                                                                                                                                    Query Match
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FILE REFERENCE: PB 0004 MO 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 15438
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 44
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AC005488.2
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                             36 SLDA 39
                                                                                                    1 SLDA 4
                                                                                                                                                                             Local Similarity
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5 SLDA 8
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn, Sharron G.
Rank, David R.
Hanzel, David K.
Chen, Wensheng
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                                                                                                                                                                                                                                                                                                                                    EXPRESSED IN BT474, SIGNAL = 3.2
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Pred. No. 2.9e+02;
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                                                                                                                                                        Mismatches
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RESULT 5
US-10-057-498-24214
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; SEQ ID NO 24214

; LENGTH: 50

; TYPE: PRT

; ORGANISM: Propioni acnes

PCT-US02-32727-24214
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Best Local Similarity
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Best Local S
Matches 4
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SEQ ID NO 54
LENGTH: 45
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                                                                                                                                                                                                                                                                            APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 70
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TITLE OF INVENTION: Compositions and Methods for Therapeutic
TITLE OF INVENTION: for Deafness, Osteoarthritis, and Abnorm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: P01899US2
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                                                                                             1 SLDA 4
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Carter, Darrick
Barth, Brenda
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Bhatia, Ajay
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; LOCATION: 33
; OTHER INFORMATION: Xaa-His or Asn
US-09-513-999C-5438
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SOFTWARE: Patent.pm
SEQ ID NO 5438
                                                                                                                                                                        Sequence 22975,
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-10-057-498-24214
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APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121-514
                                                                          APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487
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CURRENT FILING DATE: 2001-04-20
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                                               APPLICANT
                                                                                                                                                         ENERAL INFORMATION:
                APPLICANT
                                                              APPLICANT:
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TYPE: PRT
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                               APPLICANT
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                                          Wang,
                                                                          Persing, David
Bhatia, Ajay
Maisonneuve, Jean
                                          Zhang, Yanni
Wang, Siqing
Benson, Darin
                             Jen, Shyian
                odes, Michael
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                        Application PC/TUS0232727
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Pred. No. 3.5e+02;
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; ORGANISM: Propioni acnes US-10-057-498-22975
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SEQ ID NO 22375
LENGTH: 53
TYPE: PRT
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 53
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Best Local Similarity
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
APPLICANT: Douglass, John TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of FILE REFERENCE: 21012.114C1 CURRENT APPLICATION NUMBER: PCT/US02/32727 CURRENT FILING DATE: 2002-10-11
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CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514
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ORGANISM: Propioni acnes
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Carter, Darrick
Barth, Brenda
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Bhatia, Ajay
                                                                              Carter, Darrick
Barth, Brenda
                                                                                                                                                                          Zhang, Yanni
Wang, Siqing
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                                                                                                          Benson, Darin
Jones, Robert
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illarity 100.0%;
Conservative 0
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Pred. No. 3
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Pred. No. 3.5e+02
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3.5e+02;
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APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

FITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474

FILLE REFERENCE: PB 0004 WO 8

CURRENT FILLING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILLING DATE: 04 February 2000 (04.02.00)

PRIOR FILLING DATE: 05 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILLING DATE: 03 AUGUST 2000 (03.08.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR APPLICATION NUMBER: US 09/632,365

PRIOR APPLICATION NUMBER: US 09/632,365

PRIOR FILLING DATE: 03 OCTOBER 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILLING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)
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US-10-057-498-17389
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; ORGANISM: Propioni acnes
PCT-US02-32727-17389
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Matches
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CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 17389
LENGTH: 54
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11775, Application US/10203138A GENERAL INFORMATION:
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APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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Molecular Dynamics Sequence Listing Engine
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Rank, David R.
Hanzel, David K.
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Pred. No. 3.6e+02;
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PCT-US02-32727-27113; Sequence 27113, Application PC/TUS0232727; GENERAL INFORMATION:
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                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
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SEQ ID NO 2538
LENGTH: 56
TYPE: PRT
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                                                                       APPLICANT: Mitcham, Jennifer APPLICANT: Skeiky, Yasir
                                        APPLICANT:
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                           APPLICANT:
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CURRENT FILING DATE: 2002-10-11
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  APPLICANT:
                APPLICANT
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
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                                             Skeiky, Yasir
Persing, David
Bhatia, Ajay
Zhang, Yanni
Wang, Siqing
Jen, Shyian
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                                   Maisonneuve, Jean
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Jen, Shyian
                                                                                                                                                                                                                                                                                                                                                                                                                           Carter, Darrick
Barth, Brenda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benson,
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Bhatia, Ajay
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                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Darin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jennifer
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                                     Francois
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Pred. No.
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Pred, No.
                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                           3.8e+02;
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CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 27113
LENGTH: 56
TYPE: PRT
ROGANISM: Propioni acnes
US-10-057-498-27113
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US-10-057-498-2538
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US-10-057-498-2538
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LENGTH: 56
TYPE: PRT
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
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Best Local Similarity
Query Match
Best Local Similarity
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
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Barth, Brenda
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 100.0%;
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Pred. No. 3
 Score
Pred.
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18;
No.
 DB 6;
3.8e+02;
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PCT-US02-32727-27575
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PCT-US02-32727-23045
                        NUMBER OF SEQ ID NOS:
SEQ ID NO 27575
LENGTH: 57
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LENGTH: 57
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                                                      FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
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CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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TITLE OF INVENTION: Compositions and Methods
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APPLICANT: Skeiky, Yasir
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ORGANISM:
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Jen, Shyian
Lodes, Michael
Propioni acnes
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Jones, Robert
Carter, Darrick
Barth, Brenda
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Jones, Robert
Carter, Darrick
Barth, Brenda
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Bhatia, Ajay
Maisonneuve, Je
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Jen, Shyian
                                                                                                                                                                                                                              Maisonneuve, Jean
Zhang, Yanni
Wang, Siqing
                                                                                                                                                                                                Lodes, Michael
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Bhatia, Ajay
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                                                                                                                                                                                                                                                             Francois
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Pred. No. 3.8e+02;
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NAME/KBY: unsure

LOCATION: (3)

OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-498-27575
RESULT 20
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US-10-057-498-27575
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US-10-057-498-23045
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COTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-32727-27575
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 27575
LENGTH: 57
TYPE: PRT
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APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT FILING DAVID
CURRENT FILING DATE: 2001-04-20
RUMBER OF SEQ ID NOS: 29212
SEQ ID NO 23045
LENGTH: 57
TYPE: PRT
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Best Local (
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Similarity 100.0%;
4; Conservative (
                                                                                                                                                                                                                                 Conservative
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Pred. No. 3.8e+02;
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Pred. No.
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; NUMBER OF SEQ ID NOS: 30992

SEQ ID NO 28196

; LENGTH: 59

; TYPE: PRT

; ORGANISM: Propioni acnes

PCT-US02-32727-28196
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SEQ ID NO 16333
SEQ ID NO 16333
TYPE: PRT
ORGANTON
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                                                  Matches
                                                            Query Match
Best Local Similarity
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Best Local :
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121...514C1
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APPLICANT:
                                                                                                                                                                                CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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28 SLDA 31
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                       1 SLDA 4
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Ten, Shyian
Micha
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Benson, Darin
Jones, Robert
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Barth, Brenda
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Bhatia, Ajay
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Wang, Siqing
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Bhatia, Ajay
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Pred. No. 4e+02;
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RESULT 24
US-10-057-498-28196
; Sequence 28196, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
: NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 28948
LENGTH: 59
TYPE: PRT
ORGANISM: P. Acnes
PCT-US02-32727-28948
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Best Local S
Matches 4
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CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 16333
LENGTH: 59
TYPE: PRT
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Best Local Similarity
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APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
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APPLICANT:
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nes 4; Conser
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Skeiky,
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Bhatia, Ajay
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US-10-057-498-28948
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APPLICANT: Mitcham, Jennifer
APPLICANT: Skelky, Yasir
APPLICANT: Skelky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnifile Reference: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 28948
LENGTH: 59
TYPE: PRT
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Best Local Similarity
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LENGTH: 59
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Best Local
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 21639
LENGTH: 61
                                                                         APPLICANT: Jones, Robert
APPLICANT: Carter, Darrick
APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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Bhatia, Ajay
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Persing, David
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); Mismatches
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Pred. No.
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                                                                                              Diagnosis
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Sequence 7714, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: PATENT.pm
SEQ ID NO 7714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 28
US/09/513
                                                                                                                     ; OTHER INFORMATION: Xaa= *
US/09/513,999C-7714
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US-10-057-498-21639
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                                                                        Query Match
Best Local 9
                                                            Matches
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SEQ ID NO 21639
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
                                                                                                                                                                                         LENGTH: 62
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                 NAME/KEY: UNSURE
                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Propioni acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Propioni acnes
                                                     Local Similarity 100.
nes 4; Conservative
 59
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SLDA 62
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                                                                    100.0%;
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                                                    Score 18; DB 5; L
Pred. No. 4.2e+02;
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Pred. No.
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Pred. No. 4.2e+02;
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thes 0;
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                                                                                                                                                                                                                                                                                                                                                         and Encoded Human Proteins.
                                                                                Length 62;
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RESULT 30
US-10-301-997-94
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Best Local Similarity
">+ches 4; Conserv
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PCT-US02-32727-6416
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121,514C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mitcham, Jennifer APPLICANT: Skeiky, Yasir
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NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28341/33996
TELECOMMUNICATION INFORMATION: |
TELEPHONE: (312) 474-6300
                                                                                    APPLICATION NUMBER: US/09/527,431
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US/08/887,534
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           CUMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           APPLICATION NUMBER: US/10/301,997
FILING DATE: 22-NOV-2002
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
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Jen, Shyian
Lodes, Michael
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Jones, Robert
Carter, Darrick
Barth, Brenda
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Bhatia, Ajay
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Zhang, Yanni
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30992
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RESULT 31
US-10-057-498-6416
; Sequence 6416, Application US/10057498
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Best Local S
Matches 4
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SEQ ID NO 6416
LENGTH: 63
TYPE: PRT
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APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 8518
LENGTH: 65
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                              Sequence 8518, Application PC/TUS0232727
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Best Local Similarity 100.0%;
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                         APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
                                                                                                                          APPLICANT:
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INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
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les 4; Conserv
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Jen, Shyian
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                                                                                                                                       Carter, Darrick
Barth, Brenda
                                                                                                                                                                      Benson, Darin
Jones, Robert
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Bhatia, Ajay
                                                                                                                                                                                                                                                  Zhang, Yanni
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Pred. No. 4.3
0; Mismatches
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Pred. No. 4.3e+02;
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                                                                                                          for
                                                                                                          the Therapy and Diagnosis of Acnes
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1 SLDA 4

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RESULT 33
US-10-057-498-8518
; Sequence 8518, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
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Best Local Similarity
"hehes 4; Conserv:
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                                                         ; ORGANISM: Propioni acnes PCT-US02-32727-2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US02-32727-2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 8518
LENGTH: 65
TYPE: PRT
                                                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 2064
LENGTH: 68
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches
            Query Match
Best Local Similarity
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                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
                                                                                                                                                                        APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of
FILE REFERENCE: 210121.514C1
                                                                                                                                                                                                                                                      APPLICANT
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4;
                                                                                                                                                                                                                     Jen, Shyian
Lodes, Michael
Benson, Darin
Jones, Robert
Carter, Darrick
Barth, Brenda
                                                                                                                                                                                                                                                                                                                            Maisonneuve, Jean Francois
Zhang, Yanni
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Bhatia, Ajay
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Conservative
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            Score 18; DB 1;
Pred. No. 4.7e+02;
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Pred. No. 4.5e+02;
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Pred. No. 4.5e+02;
Mismatches
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Indels
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RESULT 37
PCT-US02-32727-28376
PCT-US02-32727-28376
; Sequence 28376, Application PC/TUS0232727
; GENERAL INFORMATION:
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PCT-US02-32727-6955
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US-10-057-498-2064
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APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean
APPLICANT: Zhang, Yanni
APPLICANT: Wang, Siqing
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Best Local Similarity
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SEQ ID NO 6955
LENGTH: 70
TYPE: PRT
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT APPLICATION APP
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CURRENT FILING DATE: 2002-10-11
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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APPLICANT:
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Barth, Brenda
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Jones, Robert
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Pred. No. 4.7
0; Mismatches
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RESULT 39
US-10-057-498-28376
US-10-057-498-28376, Application US/10057498
GENERAL INFORMATION:
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NAME/KEY: unsure

LOCATION: (40)

OTHER INFORMATION: Xaa =

PCT-US02-32727-28376
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US-10-057-498-6955
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SEQ ID NO 6955
LENGTH: 70
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 28376
LENGTH: 70
TYPE: PRT
ORGANISM: Propioni acnes
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
                                               APPLICANT: Mitcham, Jennifer
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APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514
                                  APPLICANT:
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
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Skeiky, Yasir
                                  Skeiky, Yasir
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Barth, Brenda
Douglass, John
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Jen, Shyian
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Jones, Robert
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Wang, Siqing
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Bhatia, Ajay
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                                                                                                                                                                                                                     Score 18; DB b; Pred. No. 4.8e+02;
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Pred. No. 4.8e+02;
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                                                                                                                                                                                                                                                      Length 70;
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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR FILING DATE: 30 AUGUST 2000 (03.08.00)
PRIOR FILING DATE: 03 LOUST 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR APPLICATION NUMBER: US 60/236, 687
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234, 687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 99/608,408
PRIOR APPLICATION NUMBER: US 99/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 15438
SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 11100
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                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION:
US-10-203-138A-11100
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US-10-057-498-28376
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CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 28376
LENGTH: 70
TYPE: PRT
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Best Local Similarity 100.0%;
Matches 4; Conservative (
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                                                                   Matches
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FILE REFERENCE: PB 0004 W0 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
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NAME/KEY: unsure
LOCATION: (40)
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                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO Z83845.14
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                               OTHER INFORMATION:
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1 SLDA 4
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                                                                                         ocal Similarity
                                                                   Conservative
                                                                                                                                                                                   SWISSPROT HIT: Q15750, EVALUE 4.00e-36
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Pred. No. 4.8
0; Mismatches
                                                                 Score 18; DB 6;
Pred. No. 4.8e+02;
); Mismatches 0;
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                                                                  ; ORGANISM: Propioni acnes PCT-US02-32727-27093
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SEQ ID NO 27093
LENGTH: 72
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LENGTH: 72
TYPE: PRT
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                                                                                                                                                              APPLICANT: Carter, Darrick
APPLICANT: Barth, Brenda
APPLICANT: Bouglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
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   Similarity 4; Conserv
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Barth, Brenda
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Lodes, Michael
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Jones, Robert
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Wang, Siqing
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Bhatia, Ajay
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Jones, Robert
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Bhatia, Ajay
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100.0%; ilarity 100.0%; Conservative 0
 Score 18; DB 1; Pred. No. 5e+02; Mismatches
                                  DB 1;
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                                Length 72;
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RESULT 45
US-10-057-498-27093
; Sequence 27093, Application US/10057498
; GEMERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
                                                                                                                                                                                                                                                                                                                                                                                RESULT 44
US-10-057-498-13114, Application US/10057498
; Sequence 13114, Application US/10057498
; GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-13114
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 210
LENGTH: 72
TYPE: PRT
ORGANISM: Lactobacillus rhamnosus
US-10-264-213-210
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US-10-264-213-210
; Sequence 210, Applica
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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APPLICANT: Havukkala, Ilka J
APPLICANT: Lubbers, Mark William
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 11000,1043c3
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
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Search completed: February
Job time : 15 secs
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NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 27093
LENGTH: 72
                                                                                                      Query Match
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Matches 4; Conserv
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         6, 2003, 11:39:03
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Minimum DB seq
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Listing first 45 s
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C86604	D72019	H72641	T34677	T06898	T17856	н87712	T41937	S19225	T35232	AH1487	AC1127	S70645	JC2403	T12686	E81786
sigma regulatory f	sigma regulatory f	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	phosphoribosyl-ATP	hypothetical prote	embryonic abundant	hypothetical prote	hypothetical prote	hypothetical prote	cell division cont	PMS8 homolog misma	hypothetical prote	conserved hypothet

ALIGNMENTS

hypothetical protein 25889 [imported] - Escherichia coli (strain O157:H7, substrain FCFENE CISPECIES: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G86126
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Maj
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Tritle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G86126
A;Accession: G86126 A;Cross-references: GB:M81443; NID:g150010; PIDN:AAA25378.1; PID:g150011 A;Note: sequence extracted from NCBI backbone (NCBIN:75202, NCBIP:75203) C;Keywords: oxidoreductase R;Chistoserdova, L.V.; Lidstrom, M.E.
J. Bacteriol. 174, 71-77, 1992
A;Title: Cloning, mutagenesis, and physiological effect of a A;Reference number: A44921; MUID:92104992; PMID:1729225
A;Contents: AM1 hydroxypyruvate reductase (EC 1.1.1.81) - Methylobacterium extorquens (fragment) C;Species: Methylobacterium extorquens C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C;Accession: A44921 Query Match Best Local Similarity Thes 4; Conserve A;Cross-references: GB:AE005174; NID:g12519291; PIDN:AAG59475.1; GSPDB:GN00145; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Gene: Z5889 A;Accession: A44921
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-20 <CHI> 밁 δÃ Matches Best Local Similarity
Matches 4; Conserv Query Match 1 SLDA 4 ||||| |12 SLDA 15 100.0%; ilarity 100.0%; Conservative (Conservative 100.0%; 0; Score 18; DB Pred. No. 63; Score 18; DB 2; Pred. No. 1.1e+02; Mismatches DB <u>ب</u> 0, Length 20 Length 33; Indels hydroxypyruvate reductas 0; Gaps 0 UWGP:

0;

Mismatches

Indels

0;

Gaps

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haptoglobin precursor - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1992 #sequence_revision 31-
                                                                HPBO
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                                                                                                                                                                           Qy
                                                                                RESULT
                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-44 <ST2>
                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005174; NID:g12513992; PIDN:AAG55329.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glas iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Z1184 [imported] -
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 1
C;Accession: E85608; F85659
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A;Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rel A;Reference number: A49410; MUID:94089752; PMID:7903455
A;Accession: D49410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 21-Sep-1994 #sequence_revision 18-Nov-1994
C; Accession: D49410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: E85608
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A; Note: sequence modified after extraction from NCBI backbone
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nilarity 100.
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Pred. No. 1.5
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Pred. No.
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thes 0;
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#text_change
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lanta, E.;
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31-Oct-1997
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K.; Apodaca
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R:Lewis, T.L.; Greenberg, n.L., ...
J. Virol. 68, 77-83, 1994
A:Title: Analysis of astrovirus serotype 1
A:Title: Analysis of A49529; MUID:94076464;
                                                                       A; Molecule type:
                                                                                                                                                                                                                                                                                                         RNA-directed RNA polymerase (EC 2.7.7.48) - human astrovirus type 1 (fragme C;Species: human astrovirus type 1 C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Dec-1994 C;Accession: B49529
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                                           A; Residues: 1-52
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A;Residues: 26.45 <Mo2>
A;Residues: 26.45 <Mo2>
C;Comment: The mature haptoglobin molecule is a dimer of heterodimers, the two chains C;Comment: Haptoglobin is a plasma glycoprotein; haptoglobin forms a complex with hem C;Superfamily: haptoglobin; complement factor H repeat homology; trypsin homology C;Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron trans F;1-25/Product: haptoglobin alpha chain (fragment) #status experimental <ALP>
F;26-45/Product: haptoglobin beta chain (fragment) #status experimental <BET>
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A; Residues: 1-49 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A40 R; Morimatsu, M.;
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       extracted
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NCBI backbone (NCBIP:141412)
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Pred. No. 1.6e+02;
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                                                                                                    conceptual translation
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No.
                                                                                                                                                                        RNA, identification of PMID:8254779
                                                                                                                                                                                                                                                                                                                                                                                                                 human astrovirus type 1 (fragment)
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                                                                                                                                                                                                                                                                             Smith, L.S.; Matsui,
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probable ribosome modulation factor rmf [imported] - Yersinia pestis (strain C;Species; Yersinia pestis C;Date: 02-Nov-2001 #senmence rowledge of the content of the conten
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C;Accession: AC2
RESULT
E86594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Title: Genome sequence of Yersinia pestis, A:Reference number: AB0001; MUID:21470413; PI
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Reference number: AB1807; MUID:21595285; PMID:11759840
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Nakazaki, 8, 205-213, 2001
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Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001;
AB0174
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Best Local
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, M.; Yasuda,
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                               hypothetical protein CP0758 [imported] - Chlamydophila pneumoniae (strain AR39) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Daci-31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: F81541 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
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RESULT 12

Brunham, R.C.; R.; Gwinn, M.;

Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O. Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.;

; Hicke Salzbe

47

SLDA

50

1 SLDA 4

Query Match Best Local

Similarity

100.0%;

Score 18; Pred. No.

DB 2; 2e+02;

Length 56;

0

0

Gaps

0;

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Genetics:

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A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; H., C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Sa Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: D81509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 28, 2311-2314, 2000

Nucleic Acids Res. 28, 2311-2314, 2000

A; Title: Comparison of whole genome sequences of chlamydia A; Reference number: A86491; MUID:20330349; PMID:10871362
A; Molecule type: DNA
A; Residues: 1-56 < REA>
A; Cross-references: GB: AEO02261; GB: AEO02161;
A; Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000; MUID:99206606; PMID:10192388 A;Accession: A72031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Chlamydophila pneumoniae, Ci
C;Date: 23-Apr-1999 #sequence_revision
C;Accession: A72031; D81509
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A; Residues: 1-56 <STO>
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R;Shirai, M.; Hiraka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CPj0831 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-56 < ARN>
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                                                                                                                                                                                                                                                                                                         \;Cross-references: GB:AE001663; GB:AE001363; NID:g4377134; PIDN:AAD18968.1; PID:g437
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Best Local S
Matches 4
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Similarity 100.0%;
4; Conservative 0
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Pred. No.
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on 23-Apr-1999 #text_o
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                            NID:g7189950; PIDN:AAF38814.1; PID:g718
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C;Accession: S24422
C;Accession: S24422
R;Shingler, V.; Powlowski, J.; Markeriol. 174, 711-724, 1992
                     A; Title: Nucleotide sequence A; Reference number: S24417; N
                                                                                                                                                        C;Species: Pseudomonas putida
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: 4-oxalocrotonate tautomerase C;Keywords: aromatic hydrocarbon catabolism; F;2-63/Product: 4-oxalocrotonate tautomerase F;2/Active site: Pro #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Comparison of the nucleotide sequences of the meta-cleavage pathway genes of cleotide substitutions contribute to enzyme evolution.
A;Reference number: S35222; MUID:93288011; PMID:8510667
A;Accession: S35225
A;Molecule type: DNA
A;Residues: 1-63 <HAR>
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A; Molecule type: DNA
A; Residues: 1-62 <REA>
A; Cross-references: GB:AE002235; GB:AE002161; NID:g7189672; PIDN:AAF38560.1; PID:g718967
                                                                                                                                                                                                                              4-oxalocrotonate tautomerase (EC 5.3.2.-)
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A;Genome: plasmid
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A; Accession:
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                     e and functional MUID:92121108; I
                                                                                                             Marklund,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Pred. No. 2.3e+02;
; Mismatches 0;
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                        analysis of the complete phenol/3,4-dimethy.
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#status predicted <MAT>
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A; Molecule type: protein
A; Residues: 34-73 < KUR>
A; Residues: 34-73 < KUR>
C; Comment: The mature haptoglobin molecule is a dimer of heterodimers, the two cha C; Comment: Haptoglobin is a plasma glycoprotein; haptoglobin forms a complex with C; Superfamily: haptoglobin; complement factor H repeat homology; trypsin homology C; Keywords: acute phase; glycoprotein; hemoglobin binding; heterotetramer; iron tr
                                                                                                                                     R:Kurosky, A.; Kim, H.H.; Touchstone, B. Comp. Biochem. Physiol. B 55, 453-459, 1976 A;Title: Comparative sequence analysis of the A;Reference number: A90931; MUID:77025019; PMI A;Accession: A26503
                                                                                                                                                                                                                                                                                                 C;Accession: A19376; A26503
R;Chow, V.; Murray, R.K.; Dixon, J.D.; Kurosky, FEBS Lett. 153, 275-279, 1983
A;Title: Biosynthesis of rabbit haptoglobin: cha;Reference number: A19376; MUID:84005090; PMID A;Accession: A19376
                                                                                                                                                                                                                                                                                                                                                                                                                           N;Contains: haptoglobin alpha chain; haptoglobin beta chain C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 31-Mar-1988 #seguence_revision 31-May-1996 #text_ch
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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A; Molecule type: DNA
A; Residues: 1-63 <SHI>
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A; Residues: 1-64 <STO>
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Best Local
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Pred. No. 2.3e+02;
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A;Molecule type: DNA
A;Residues: 1-75 <REA>
A;Cross references: GB:AE002238; GB:AE002161;
A;Experimental source: strain AR39, HL cells
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70523
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                                                                                                                                                                                                                  A;Title: Genome sequences of Chlamydia trachomatis MoPn A;Reference number: A81500; MUID:20150255; PMID:10684935 A;Accession: A81539
                                                                                                                                                                                                                                                                Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                          exodeoxyribonuclease, small chain CP078 (Species: Chlamydophila pneumoniae, ChC; Species: AMAr-2000 #sequence_revision C; Accession: A81539
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A; Residues: 1-73 <COL>
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4; Conservative
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4; Conser
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R.; Gwinn, M.; Nelson, W
Res. 28, 1397-1406, 2000
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                                                          Conservative
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ce: strain |
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H37Rv
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Pred. No.
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31-Mar-2000 #text_change 11-May-2000
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R;Tomaschewski, J.; Rueger, W. Nucleic Acids Res. 15, 3632-3633, 1987 Nucleic Acids Res. 15, 3632-3633, 1987 A;Reference number: A30291; MUID:87203398; PMID:3575111 A;Accession: F30292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
G83935
                                                                                                                A; Note: host Escherichia coli
C; Date: 31-Dec-1989 #sequence_revision
C; Accession: F30292
                                                                                                                                                                   gene 55.1 protein
C; Species: phage 1
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-85 <KLE>
A; Cross-references: GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The complete genome sequence of the hyperthermophilic, A;Reference number: A69250; MUID:98049343; PMID:9389475 A;Accession: A69435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs,
Smith, H.O.; Woese, C.R.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Archaeoglobus fulgidus
C; Date: 05-Dec-1997 #sequence_revision
C; Accession: A69435
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A; Title: Complete genome sequence of the alkaliphilic bacterium A; Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision
C;Accession: G83935
R;Takami, H; Nakasone, K; Takaki, Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thioredoxin related protein BH2287 [imported] - Bacillus halodurans C; Species: Bacillus halodurans
A; Molecule type:
A; Residues: 1-87
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A; Residues: 1-76 <STO>
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llarity 100.0%;
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Pred. No. 2.8
0; Mismatches
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3.; Gill, S.; Kirkness,
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GB:Y00122;

NID: g15346; PIDN: CAA68320.1;

PID:g15362

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                                                                                                                                                                                                                                                                                                                 R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                     hypothetical protein AGR_C_187 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: B97373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: E84162

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berguist, B.; Pan, M.; Shukla, H.D.; Lasky, J. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab Jung, K.H.; Alam, M.; Freitas, T. Jung, K.H.; Alam, M.; Freitas, T. Jung, K.H.; Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: E84162
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A;Gene: 55.
C;Superfami
                                                                                                                                                                   A;Map
                                                                                                                                                                                                                            A; Molecule type: DNA A; Residues: 1-88 < KUR>
                                                                                                                                                                                                                                                       A;Status: preliminary
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C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-87 <STO>
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24
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tes 4; Conserv
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4; Conservative
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Pred. No.
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Pred. No. 3.2e+02;
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3.3e+02;
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; Scott, C.; Lappas, C.;
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Markelz, B.
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R; Dong, J.Z.; Dunstan, D.I. submitted to the EMBL Data Library,
                                                                                                                                                     embryonic abundant protein EMB44 - white spruce C;Species: Picea glauca (white spruce) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1-C;Accession: T09285
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C; Superfamily:
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C;Accession: AB2591
C;Accession: AB2591
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, 1., Took and the series of the s
A; Reference number: A; Accession: T09285
                                                           A; Description:
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A; Residues: 1-88 <KUR>
A; Cross-references: GB:AE008688; PIDN:AAL41144.1;
A; Cross-references: Strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-90 < PRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Bordetella pertussis
C;Date: 21-Jan-2000 #sequence_revision
C;Accession: T44780
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A;Map position: circular
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C;Date: 11-Jan-2002 #sequence_revision |11-Jan-2002 #text_change 11-Jan-2002
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Best Local
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mber: Z16588
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Pred: No. 3.3e+02;
Pred: No. 3.3e+02;
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ng somatic
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Mismatches
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preliminary;

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GB/EMBL/DDBJ

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C;Accession: E81209

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein NMB0343 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - white spruce (Species: Picea glauca (white spruce) C; Species: Picea glauca (white spruce) C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 C; Accession: T09293 R; Dong, J.Z.; Dunstan, D.I. Planta 199, 459-466, 1996
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A; Residues: 1-91 <DON>
A; Cross-references: EMBL:L47750; NID:g1350537; PID:g1350538
C; Genetics:
A; Gene: EMB44
C; Superfamily: embryonic abundant protein Em
                                                                                                                                                                                                                                                         A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; MA;Title: Complete genome sequence of Neisseria meningitidis A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: E81209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Expression of abundant mRNAs during somatic embryogenesis A;Reference number: Z16636; MUID:96367688; PMID:8771802 A;Accession: T09293
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C;Superfamily: embryonic
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A; Residues: 1-91 <DON>
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A; Experimental source: serogroup
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A; Residues: 1-92 <TET>
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Best Local :
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B, strain MC58
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Pred. No. 3.4e+02;
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hypothetical protein 63B12.12 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-C;Accession: T12686 R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G. submitted to the EMBL Data Library, January 1998 A;Description: Sequencing the distal X chromosome of Drosophila melasteference number: Z17572
                                                                                                                                                                                                                              RESULT
T12686
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T10931
                                                      A; Reference number: A; Accession: T12686
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A; Residues: 1-96 < PAR>
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C;Date: 05-May-2000 #sequence_revision 05-May-2000
C;Accession: E81786
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A;Accession: T10931
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A; Molecule type: DNA
A; Residues: 1-96 <FER>
                                  A; Status: preliminary; translated
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily:
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source: strain A3(2)
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                    #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                      from
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Pred. No. 3.6e+02;
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August 1998
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                                                                                              of Drosophila melanogaster
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Mungall, K.; Quail,
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M.A.;
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Rajandre
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EMBL:AL021106; NID:e1371406; PID:e1226203; PIDN:CAA15943.1

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cell division control protein CKS1 - Leishmania mexicana N;Alternate names: protein pl2LmmCKS1; protein pl3sucl homolog C;Species: Leishmania mexicana C;Date: L4-Feb-197 #sequence_revision 13-Mar-1997 #text_change C;Date: 14-Feb-197 #sequence_revision 13-Mar-1997 #text_change C;Date: 14-Feb-197 #sequence_revision 13-Mar-1997 #text_change C;Date: J4-Feb-197 #sequence_revision 13-Mar-1997 #sequence_revision
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                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: Z49881; C; Genetics:
                                                                                                                                                                                                                                                                             A; Gene: cks1
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A;Cross:references: GDB:437147
A;Map position: 7q11.23-7q22
C;Keywords: DNA repair
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R;Horil, A.; Han, H.J.; Sasaki, S.; Shimada, M.; Nakamura, Y. Biochem. Biophys. Res. Commun. 204, 1257-1264, 1994
A;Title: Cloning, characterization and chromosomal assignment of A;Reference number: JC2398; MUID:95071462; PMID:7980603
A;Accession: JC2403
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A; Residues: 1-98 <HOR>
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A;Introns: 27/1
A;Note: 63B12.12
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                                                                                                        Matches
                                                                                                                                                                                                                Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Homo sapiens (man)
;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 05-Nov-1999
;Accession: JC2403
                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                          Superfamily:
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SLDA 14
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4; Conservative
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                                                                                                        Conservative
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Pred. No. 3.7e+02;
Pred. No. 3.7e+02;
                                                                                                                               Pred.
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Pred. No.
                                                                                               Mismatches
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hypothetical protein SC5C7.25 SC5C7.25 - Streptomyc C; Species: Streptomyces coelicolor C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999
                      R; Seeger, K.J.; Harris submitted to the EMBL
                                                                                                                                                    RESULT
T35232
                                                                 C; Accession:
                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein lin0439 [imported] Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Species: Listeria innocua C;Species: Listeria innocua C;Cate: 27-Nov-2001 #sequence_revision 2/-Nov-2001 #text_change 27-Nov-2001 C;Accession: AH1487 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D. D.; Jones, L.M.; Karst, U.
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    A;Reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-99 <GL
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1127
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A; Residues: 1-99 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:NC_003210; PIDN:CAC98497.1; PID:g16409795; GSPDB:GN00177A;Experimental source: strain EGD-e
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Best Local S
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K.J.; Harris, D.;
to the EMBL Data
ce number: Z21572
                                                                                                                                                                                                                                                                                                                         Similarity 4; Conserv
                                                                   T35232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <GLA>
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                                             D.,
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                    Library,
                    Parkhill, J.; Barrell,
Library, September 1998
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                                                                                                                                                                                                                                                                                                                  Score 18; DB z;
Pred. No. 3.7e+02;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DE Pred. No. 3.7); Mismatches
                                                                                                                         Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; 1
3.7e+02;
les 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pkat, G.; Madueno, E.;
Vazquez-Boland, J.A.;
                                    B.G.; Rajandream, M.A.
                                                                              #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                             Length
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Voss, H.; Wehla
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Fsihi,
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submitted to the EMBL Data Library, December 1995
A;Description: Determination and analysis of the col
A;Reference number: 222022
A;Accession: T41937
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-104 <NIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-102 <BAKI>
A;Cross-references: EMBL:X13205; NID:g18493; PIDN:CAA31593.1; PID:g18494
A;Cross-references: EMBL:X13205; NID:g18493; PIDN:CAA31593.1; PID:g18494
R;Baker, J.; Steele, C.; Dure III, L.
R;Title: Sequence and characterization of 6 Lea proteins and their genes from cotton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 31-Mar-1992 #sequent
C;Accession: S19225; S04041
R;Dure III, L.S.
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S19225
A; Experimental source: strain JI C; Genetics: A; Note: U35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-101, 'KLNIISHDRTLATPFIYKP'
A; Cross references: EMBL: X13205
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                                                                                                                                                                                                                     R; Nicholas, J.
                                                                                                                                                                                                                                        C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T41937
                                                                                                                                                                                                                                                                               C;Species: human herpesvirus A;Variety: strain JI
                                                                                                                                                                                                                                                                                                        hypothetical protein U35 - human herpesvirus C. Species: human herpesvirus 7
                                                                                                                                                                                                                                                                                                                                                RESULT 38
T41937
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A; Accession: S04041
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                                                          A; Cross-references: EMBL: U43400; PIDN: AAC54697.1
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Gene: SCOEDB:SC5C7.25
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Best Local
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Matches 4; Conser
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Best Local
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Pred. No.
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Pred. No.
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3.9e+02;
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hes 0;
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RESULT 40
T17856
hypothetical protein 108 - Cyanophora paradoxa cyanelle C;Species: cyanelle Cyanophora paradoxa C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #texic;Accession: T06898
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H87712
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R;Graves, M.V.; Van
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C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Experimental source: specific host Chlorella strain NC64A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z18806
A; Accession: T17856
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A; Residues: 1-107 <STO>
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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C;Accession: H87712
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C;Species: Caulobacter crescentus
                                                                                                                                                                RESULT 41
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Pred. No.
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Pred. No. 3.9e+02;
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Bohnert,

H.J.; Bryant, D.A.

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awa, H.; Takamiya, M.; Masuda, S.; Fundanda, A.; Takamiya, I.)
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72641
A;Status: preliminary
                                                                               A; Status: A: DNA
A; Molecule type: DNA
A; Residues: 1-109 KKAW>
A; Cross-references: DDBJ: AP000060;
A; Cross-references: Strain Kl
                                                                                                                                                                                                                                                   R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; awa, H.; Takamiya, M.; Masuda, S.; Funahash
                                                                                                                                                                                                                                                                                      hypothetical protein APE0568 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: H72641
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T34677
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submitted to the EMBL Data Library, July 1995
A;Description: Nucleotide sequence of the cyanelle genome
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-108 <SAU>
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A; Accession: T34677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SC1A9.28c SC1A9.28c - Streptomyces coelicolor
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A; Residues: 1-108 <STI>
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Gene: SCOEDB:SC1A9.28c
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llarity 100.0%;
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ce: strain Pringsheim LB555
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Pred. No.
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                                                                                                                                                                                                                                                 kawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak:
Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
                                                                                                        NID:g5104188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:CAA22398.1; GSPDB:GN00070; SCOEDB:SC1A9.28c
 Score 18;
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C; Superfamily:
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A;Title: Comparison of whole genome sequences of chlamydia A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                 sigma regulatory factor [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
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C;Superfamily:
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A; Molecule type: DNA
A; Residues: 1-110 <ARN>
A; Cross-references: GB: AE001671; GB: AE001363;
A; Cross-references: Strain CWL029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000; MUID:99206606; PMID:10192388 A;Accession: D72019
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C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
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                                                                                                                                                                                             A;Cross-references: GB:BA000008; NID:g8979283; A;Experimental source: strain J138
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-110 <STO>
                                                                                                                                                                                                                                                                                                                                                                    C; Accession: C86604
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                               A; Accession: C86604
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Listing first 45 summaries
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Y04A_BPT4
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ES98_DROME
CKS1_LEIME
PHS_STRCO
LE19_GOSHI
H152_CAUCR
YC50_CYAPA
ACEW_SCHPO
SEP3_BOVIN
Y998_RHIME
YE06_HAEIN
CHH4_PENMO
RL22_HELPJ
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RL22_HELPJ
RL22_HELPJ
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Y111_MYCLB
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Compugen Ltd
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P4917 pseudomonas
Q01468 pseudomonas
Q01464 chlamydia p
Q48410 bacteriopha
Q28790 archaeoglob
P07083 bacteriopha
Q40864 picea glauc
Q86655 streptomyce
Q97420 drosophila
Q86722 streptomyce
P09443 gossypium h
Q9a228 caulobacter
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Q01479
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7 mycobacteri
4 bos taurus
4 mycobacteri
2 saccharomyc
2 triticum ae
3 triticum ae
7 caenorhabdi
2 yersinia pe
                                                                                                                           6 cyanophora
7 schizosacch
7 bos taurus
6 rhizobium m
1 haemophilus
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helicobacte
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xylella fas
triticum ae
herpes simp
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DI DI AC

DMPI_PSESP STANDARD: PRT; 62 AA. P49172; 61 PFB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)

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RESULT 2	5 1	Query Ma Best Loc Matches								T_T SU		888844444 4888948
SESP CHARLES THE CO.	es 4; Conservative 0; Mismatches 1 SLDA 4 5 SLDA 8	Match 100.0%; Sc Cocal Similarity 100.0%; Pr Es 4; Conservative 0;	otease_Try. DOM; PARTIAL. asma; Hemoglobin-bi 215B2003101B7B84	IN PLASMA. - SIMILARITY: THE BET BUT HAPTOGLOBIN HAS POSITIONS CORRESPON PROTEASES ARE OCCUP PROTEASES ARE 0CCUP A26503.	ACCESSIBLE TO DEGRADATIVE ENZYMES. - SUBGUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CI- SUBGELLULAR LOCATION: EXCERCELLULAR. - TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER,	dg haptoglobin beta-chain n. Physiol. 55B:453-459(19 : HAPTOGLOBIN COMBINES WII IN THROUGH THE NG LOSS OF IRON THROUGH THE FROM DAMAGE BY HEMOGLOBIN,	[1] SEQUENCE. SEQUENCE. MEDLINE=77025019; PubMed=975782; Kurosky A., Kim H.H., Touchstone B.; "Comparative secuence analysis of the N-termina	yus cuniculus (Rabbit). 3; Metazoa; Chordata; Craniata; Ver 5: Eutheria; Lagomorpha; Leporidae; 1D-9986;	01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) Haptoglobin beta chain (Fragment).	RABIT STANDARD; P	ALIGNMENTS	18 100.0 144 1 PSB2_ECOLI 18 100.0 147 1 HEAA_CAUCR 18 100.0 147 1 RS12_SULSO 18 100.0 147 1 RS12_SULSO 18 100.0 147 1 RS12_SULTO 18 100.0 150 1 TPCB_HOMAM 18 100.0 150 1 TPCB_HOMAM 18 100.0 151 1 RS12_SULAC 18 100.0 151 1 RS12_SULAC 18 100.0 151 1 Y4JR_RHISN 18 100.0 154 1 COBE_PSEDE 18 100.0 154 1 COBE_PSEDE 18 100.0 157 1 UATL_HELVI 18 100.0 157 1 UATL_HELVI 18 100.0 157 1 UL51_HCMVA 18 100.0 150 1 RISB_MYCTU
		Length 40; Indels 0; Gaps	nding; Liver. CRC64;	D TO SERINE PROTEASES, PROBABLY BECAUSE THE COTIVE SITE RESIDUES IN LIDS IN HAPTOGLOBIN.	INS.	HEMOGLOBI PROTECTIN		tebrata; Euteleostomi; Oryctolagus.				P10032 escherichia P27342 caulobacter P39573 sulfolobus Q976a8 sulfolobus Q976a8 sulfolobus P29291 homarus ame Q9hvz4 pseudomonas P11524 sulfolobus P55518 rhizobium s P21635 pseudomonas P55277 heliothis v P16792 human cytom P71685 mycobacteri

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01-JUL-1993
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                                                    Bacteria; Proteobacteria;
                                                                           Pseudomonas
                                                                                                4-oxalocrotonate tautomerase
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        SEQUENCE FROM N.A.,
                                           Pseudomonas
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modified and this statement is not remove
entities requires a license agreement (Sonor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson K.S., Wigley D.B.;
"Enzymatic ketonization of 2-hydroxymuconate: specificity and mechanism investigated by the crystal structures of two isomer Blochemistry 35:792-802(1996).

FUNCTION: CATALYZES THE KETONIZATION OF 2-HYDROXYMUCONATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pVI150.
Bacteria; Protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                   ProDom; PD019232; Tautomerase; 1.
TIGRFAMs; TIGR00013; taut; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Subramanya H.S., Roper D. Wilson K.S., Wigley D.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X60835; CAA43229.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence and functional phenol/3,4-dimethylphenol catabolic strain CF600.":
                                                                                                                                                                                                                                                                                                                                           somerase;
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Similarity 100.0%;
4; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                           Tautomerase; 1.
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38,
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    AND SEQUENCE OF 1-33
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0 BY SIMILARITY.
1 CATALYTIC BASE (BY SIMILARITY).
6974 MW; CEDABOF92D1E1E0F CRC64;
                                                                                          Last sequence update)
Last annotation update)
omerase (EC 5.3.2.-) (4-OT).
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Powlowski J.;
functional analysis of the complete
control of pathway of Pseudomonas sp.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEGRADATION OF TOLUENE
                                                Pseudomonadaceae;
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Query Match
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                                                                                            INIT_MET ACT_SITE
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR, AND ACTIVE SITE.
MEDLINE-9616413; PubMed-8547260;
Stivers J.T., Abeygunawardana C., Mildvan A.S.
Whitman C.P., Chen L.H.;
"Catalytic role of the amino-terminal proline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: CATALYZES THE KETONIZATION OF 2-HYDROXYMUCONATE STEREOSELECTIVELY TO YIELD 2-OXO-3-HEXENEDIOATE.
-!- PATHWAY: META-CLEAVAGE PATHWAY, FOR THE DEGRADATION OF TOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxo-3-pentynoate at 2.4-A resolution: analysis the mechanism of inactivation and catalysis."; Biochemistry 37:14692-14700(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tautomerase: affinity labeling Biochemistry 35:803-813(1996).
                                                                                                                                    Somerase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mechanism investigated by the crystal Biochemistry 35:792-802(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Subramanya H.S., Roper D.I., Dauter Z., Dodson Wilson K.S., Wigley D.B.; "Enzymatic ketonization of 2-hydroxymuconate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harayama S., Rekik M.;
"Comparison of the nucleotide sequences of the meta-cleavage pathway genes of TOL plasmid pwW0 from Pseudomonas putida with other meta-cleavage genes suggests that both single and multiple nucleotide substitutions contribute to enzyme evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor A.B., Czerwinski R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98453316; PubMed=9778344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Crystal structure of 4-oxalocrotonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96146412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Gen. Genet. 239:81-89(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen L.H., Kenyon G.L., Curtin
Hajipour G., Whitman C.P.;
"4-oxalocrotonate tautomerase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93288011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-mt-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residues
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Chen L.H., Kenyon G.L., Curtin F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: META-CLEAVAGE PATHWAY FOR M-XYLENE AND P-XYLENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMOHEXAMER.
                                                                                                                                                                                 PD019232;
                                                                                                                                                    TIGR00013; taut;
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                                                                                                           Plasmid; Aromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    per monomer."
                                                                       62
                                                                     ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267:17716-17721(1992).
                                                                                                                                                                        Tautomerase; 1.
                                                                   6811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8547259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8510667;
100.0%;
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                                                                     Ϋ́
                                                            CATALYTIC BASE.
23E6DC494A12254F CRC64;
                                                                                                                                hydrocarbons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dodson E.J.,
                                                                                                                             catabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jr.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4-oxalocrotonate NMR studies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bembenek M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 62
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                                                                                                                         3D-structure.
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Matches

Local

Similarity 4; Conserv

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Gaps

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Score 18; Pred. No.

No. 1.2e+02;

DB 1;

Length

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RESULT 4
EX7S_CHLPN
                                       EMBL; AE001686; EMBL; AE002238; AE002548; EMBL; AP002548; TIGR; CP0788; -
                                                                                                                                                                                                                                  Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. tra Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII small subunit
(Exonuclease VII small subunit).
XSEB OR CPMI061 1 OR CP0788.
                                                                                                     use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gwinn M., Nelson W., DeBoy R., Kolonay J.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg
White O., Hickey E.K., Peterson J., Utterback T., Berry
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EX7S_CHLPN
Q9K1Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C.,
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20330349; PubMed-10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                             SUBCELLULAR SIMILARITY:
IPR003761; Exonuc_VII_S
2609; Exonuc_VII_S; 1.
TIGR01280; xseB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                -; NOT_ANNOTATED_CDS.
AAF38587.1; -.
                                                                                                                                                                                                             LOCATION: Cytoplasmic (By similarity). BELONGS TO THE XSEB FAMILY.
                                                    -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MoPn
                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Chlamydia
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                                                                                                                                                        restrictions
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y K., Bass S.,
, Dodson R.,
, Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyman R.W.,
                                                                                                                                  and
                                                                                                                                                                   EMBL outstation
                                                                                                                                                                                   a collaboration
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GP56,BSP1

ID GP56,B

AC 048410

AC 048410

DF 15-DEC

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ON SEQUEN

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16-0CT-2001
16-0CT-2001
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MEDILINE-98327781; PubMed=9657951;

Stewart C.R., Gaslightwala I., Hinata K., Krolikowski K.A.,

Needleman D.S., Peng A.S.-Y., Peterman M.A., Tobias A., Wei P.,

"Genes and regulatory sites of the 'host-takeover module' in the

"genes and redundancy of Bacillus subtills bacteriophage SPO1.";
              SEQUENCE FROM N.A. STRAIN-VC-16 / DSM 4304 / ATCC 49 MEDLINE-98049343; PubMed-9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                             Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeog
Archaeoglobaceae; Archaeoglobus
NCBI_TaxID=2234;
                                                                                                                                                                                                             Hypothetical AF1482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF031901; AAC29025.1;
Hypothetical protein.
SEQUENCE 79 AA; 9305 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage SP01.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Nuclease; Exonuclease; Complete proteome SEQUENCE 75 AA; 8809 MW; AA05874AFFA83728 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 246:329-340(1998).
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15-DEC-1998
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(Rel. 37, Last sequence up
(Rel. 37, Last annotation
ne protein 56.
                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
L protein AF1482.
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Pred.
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White O.,
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1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 79;
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  Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 7
Y04A_BPT4
ID 4704A
AC P0708
AC P0708
DT 01-AF
DT 15-JU
DE Hypot
GN Y04A
OS Bacte
OC T4-ILI
OX NCBI.
RN SEQUI
RC STRA
RX TOMBLI
RN [2]
RN [2]
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RN SEQUI
RA MESY
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Best Local :
use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P07083;
01-APR-1988
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic
[2]
                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              Kutter E., Arisaka F., Kunisawa T., Tsugita A
Mesyanzhinov V., Ruger W., Stidham T., Thomas
"Bacteriophage T4 genome analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 9.8 kDa protein in Gp55-nrdG intergenic region.
704A OR 55.1.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence and primary structures of gene products coded for by the T4 genome between map positions 48.266 kb and 39.166 kb Nucleic Acids Res. 15:3632-3633(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage T4.
Viruses; dsDNA viruses,
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87203398; PubMed=3575111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001000; AAB89770.1; TIGR; AF1482; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S. Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zho Overbeek R., Goozayne J.D., Weidman J.F., McDonald L., Utterback Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ľomaschewski J., Rueger W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nature 390:364-370(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; TRANSMEM 12 3
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ilarity 100.0%;
Conservative (
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4 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no
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1E2C08D875699B65 CRC64;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caudovirales; Myoviridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
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ches 0;
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There are no restrictions
ng as its content is in
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RESULT 9
RS15_STRCO
ID RS15_S
AC 086655
AC 086655
DT 30-MAY
DT 15-JUN
DE 30S r1
GN RPSO 0
OS Strept
OC Bacter
OC Actino
OX NCBI_T
RN [1]
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ID EML_P
AC 04086
DT 01-NO
DT 01-NO
DT 01-NO
DE Em-li
OS Picea
OC EMACH
OX NCBI_
RN [1]
RN [1]
RP SEQUE
RP SUBMI
CC -1-S
CC This
CC 
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Best Local S
Matches 4
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Best Local S
Matches 4
                                                                                                                                                     RS15_STRCO STANDARD, 086655; 30-MAY-2000 (Rel. 39, C. 30-MAY-2000 (Rel. 39, L. 15-JUN-2002 (Rel. 41, L. 15-JUN-2002 (Rel. 41, L. 15-JUN-2002 (Rel. 41, L. 15-JUN-2002)
                                                                        Streptomyces coelicolor.
Bacteria; Actinobacteria
                                                                                                                 30S ribosomal protein S15. RPSO OR SC05736 OR SC3C3.22.
                          Actinomycetales; Streptomycineae;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMI_PICGL STANDARD; PRT; 91 AA. Q40864; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000389; Seed_protein.
pfam; PF00477; seed_protein; 1.
prOSITE; pS00431; SMALL_HYDR_PLANT_SEED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L42464; AAA85366.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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Dong J.Z., Dunstan D.I.;
Submitted (JAN-1996) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Picea glauca (White spruce).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
NCBI_TaxID-3330;
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EMBL; AF158101; AAD42492.1;
PIR; F30292; ZGBPT9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                 1 SLDA 4
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                                                              Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryo.
91 AA;
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7 AA; 9845 MW;
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9771 MW;
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                                                                                                                                                            Last annotation
                                                                                                                                                                                                            Created)
                                                                                                                                                                                    Last sequence
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THE SMALL HYDROPHILIC PLANT
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Pred. No. 1.9e+02;
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Pred! No.
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                                           Streptomycetaceae;
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                                                                                                                                                            update)
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                                      Streptomyces
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RESULT 10
ES98_DROME
ID 8598_DROME
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AC 09742
DT 15-JU
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SERVINES REPRESENTATION OF THE PROPERTY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nature 417:141-147(2002).
-I- FUNCTION: THIS PROTEIN IS ONE PROTEINS (BY SIMILARITY).
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
EST00098 protein homolog.
EG:63B12.12 OR CG14818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005290; RS15_bact.
InterPro; IPR00589; Ribosomal_S15.
InterPro; IPR000589; Ribosomal_S15; 1.
FIGREAMS; TIGR00952; S15_bact; 1.
PROSITE; PS00362; RIBOSOMAL_S15; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
Ribosomal protein; rRNA-binding; Complete CRC64;
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Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ES98_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
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Similarity 100.0%;
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Neoptera; Endopterygota; Diptera; Brachycera;
Oidea; Drosophilidae; Drosophila.
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Pred. No. 1.9e+02;
; Mismatches 0;
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                                                                                                                                       RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McRavillov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Molson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Schence 287:2185-2195(2000).
                                              Query Match
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Matches 4
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STRAIN-Oregon-R;

MEDLINE-20196011; PubMed-10731137;

MEDLINE-20196011; PubMed-10731137;

Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,

Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu I

Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova

Minana B., Kafatos F.C., Louis C., Siden-Klamos I., Bolshakov S.,

Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,

Modolell J., Peter A., Schoettler P., Werner M., Mourkloti F.,

Beinert N., Dowe G., Schaefer U., Jacekle H., Bucheton A.,

Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,

Glover D.M.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandr Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Du Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein;
DOMAIN 21 7
                                                                                                                                                                                                                        FlyBase; FBgn0026088; EG:63B12.12. InterPro: IPR005374; UPF0184.
                                                                                                                                                                                                                                                                    EMBL; AE003422; AAF45682.1; -. EMBL; AL021106; CAA15943.1; -.
                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as are not removed. Its in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                      Pfam; PF03670; UPF0184;
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98452A2233F231BF CRC64;
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                                                Mismatches
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Best Local
                                                                                                        Streptomyces coelicolor.

Streptomyces coelicolor.

Bacteria; Actinobacteria; Actinobacteridae;

Partinomucetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                        PHS_STRCO STANDARD; PRT; 101 AA.

086722;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) (PHS)
(4-alpha-hydroxy-tetrahydropterin dehydratase) (Pterin carbinolamine dehydratase) (PCD)
  STRAIN-A3(2) / M145;
MEDLINE-21996410; Pu
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                SC06540 OR SC5C7.25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00296; CYCLINKINASE.
ProDom; PD005152; Cyc_dep_kin_rsub;
PROSITE; PS00944; CKS_1; 1.
PROSITE; PS00945; CKS_2; 1.
Cell division.
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Pfam; PF01111; CKS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z49881; CAA90037.1; -. HSSP; P33551; 1BUH.
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"Leishmania mexicana p12cks1, a homologue of associates with a stage-regulated histone H1 Biochem. J. 316:833-839(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cyclin-dependent kinases regulatory subunit (P12LMMCKS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=M379 / MNYC
MEDLINE=96265049; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania mexicana.
Eukaryota, Euglenozoa, Kinetoplastida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKS1_LEIME Q25330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: BINDS TO THE CATALYTIC SUBUNIT OF THE CYCLIN DEPENDENT KINASES (CDC2) AND IS ESSENTIAL FOR THEIR BIOLOGICAL FUNCTION. SUBUNIT: FORMS AN HOMOHEXAMER THAT CAN PROBABLY BIND SIX KINASE SUBUNITS (BY SIMILARITY).

SIMILARITY: BELONGS TO THE CKS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLDA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11832 MW;
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100.0%; F
itive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 1;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5F2C766A69AD5222 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
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kinase.";
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RESULT 13
LE19_GOSHI
ID LE19_GOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
SEQUENCE FROM N.A.
Galau G.A., Wang H.Y., Hughes D.W.;
Galau G.A., Wang H.Y., Hughes D.W.;
Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: LEA PROTEINS ARE LATE EMBRYONIC PROTEINS ABUNDANT
HIGHER PLANT SEED EMBRYOS. THERE ARE TWO SUBSETS OF LEA PROT
                                                                                                                                                         Dure L. II Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gossypium hirsutum (Upland cotton).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P09443;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
                                                                                                                                                                                                                                                                                      cotton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OI-JUN-1994 (Rel. 29, Last annotation update)
Late embryogenesis abundant protein D-19 (LEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).

'I CATALYTIC ACTIVITY: (6R)-6-(L-erythro-1,2-dihydroxypropyl)-5,6,7,8-tetrahydro-4a-hydroxypterin = (6R)-6-(L-erythro-1,2-dihydroxypropyl)-7,8-dihydro-5H-pterin + H(2)O.

-!- SIMILARITY: BELONGS TO THE PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                          Plant
                                                                                                                                                                                                                                                                                                                                    Baker J.,
                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3635;
                                                                                                                                                                                                            REVISIONS
                                                                                                                                                                                                                                                                                                        "Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 1(
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Pfam; PF01329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL031515; CAA20637.1; HSSP; P80095; 1DCO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M. Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S. Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch F. Batandraga V. B., Bethologies G. B., Collins M. C. Collins M. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentley S.D., Thomson N.R.,
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                                                                                                                                                                                                                                                            Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F01329; Pterin_4a; 1.
PD007262; Trans_pterinDh; 1
tical protein; Lyase; Comple
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                                                                                                                                                                                                                                                                                                  Steele C., Dure L. II and characterization
                                                                                                                                                                                                                                                                                                                            . Coker 201;
Steele C., I
                                                                                                                                                         (JAN-1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001533; Trans_pterinDh.
                                                                                                                                                                                                                                                       Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                    11:277-291(1988)
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; DB175F371A11C159 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 1;
Pred. No. 2.1e+02;
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Howarth S.,
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OF LEA PROTEINS

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RESULT 14
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Q9A228
DT 15-JUN
DT CAULOB
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Best Local
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EMBL; X13205; CAA31593.1; -.

EMBL; M73751; AAA33062.1; -.

EMBL; M73752; AAA33060.1; -.

PIR; S19225; S19225.

InterPro; IPR000389; Seed_protein.

Pfam; PF00477; seed_protein; 1.
                                                                                                                                                                                                                    Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

-i- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + diphosphate.

-i- PATHWAY: Histidine biosynthesis; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seed; See
SEQUENCE
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between
                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed-11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIS2_CAUCR Q9A228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00431; SMALL_HYDR_PLANT_SEED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Phosphoribosyl-ATP pyrophosphatase (EC 3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 SLDA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SLDA 4
             European Bioinformatics Institute.
by non-profit institutions as leading and this statement is not removed.
                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE PRA-PH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (5A, AND 5B), THE FIRST ONES ARE EXPRESSED WHEN THE WEIGHT REACH 80 MG AND THE SECOND SET ARE EXPRESSED THE FUNCTION OF THOSE PROTEINS IS NOT KNOWN.
INDUCTION: BY ABSCISIC ACID (ABA).
MISCELLANEOUS: THIS IS A SET 5B PROTEIN.
SIMILARITY: BELONGS TO THE SMALL HYDROPHILIC PLANT SET STATEMENT STATEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR CC3738.
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4; Conserv
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FCC74BEF167ECD27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 3.6.1.31) (PRA-PH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
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hes 0;
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is
1 for
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M., White O.,
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40 SLDA 43

1 SLDA 4

Matches

Similarity

100.0%;

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Score 18; DB 1; Pred. No. 2.2e+02; Mismatches 0;

Length 108; CRC64

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Gaps

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108

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Best Local S
Matches 4
                                                                                                                                                                               STRAIN-LB555 / Pringsneim;
STRAIN-LB555 / Pringsneim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., A., Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Aller Rarley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C., Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
The complete sequence of the cyanelle genome of Cyanophora the genetic complexity of a primitive plastid.";
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
Schwemmler W. (eds.);
Schwemmler W. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996
01-FEB-1996
16-OCT-2001
Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histidine biosynthesis; Hydrolase; Complete proteome. SEQUENCE 107 AA; 11037 MW; 93280F1FAA8629ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01503; PRA-PH; 1. ProDom; PD002611; PRA-PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006031; AAK25700.1; -. TIGR; CC3738; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a or send an email to
                          EMBL; U30821; AAA81241.1; -
                                                       or send
                                                                     entities requires a
                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Bryant D.A.;
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=LB555 / Pringsheim;
Stirewalt V.L., Michalowski C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyanelle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyanophora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P48326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002497;
                                                                                                                                                                                                                                                                                                                                                     Plant Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2762;
                                                                                                                                                                    -! - SIMILARITY: BELONGS TO THE YCF50 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 SLDA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SLDA 4
                                                                                                                                                                                                                                                                                                                                                    leotide sequence of the cyanelle DNA from Cyanophora paradoxa."; t Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYAPA
                                                    s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glaucocystophyceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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(Rel.
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             protein;
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40,
kDa
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              Cyanelle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
protein ycf50 (ORF108).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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Pred. No. 2.2
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyanophoraceae;
                                                                                                                                                                                                                                                                                                                                                                                            Loeffelhardt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                            There are no restrictions ong as its content is in
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                                                                               Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyanophora
                                                                                                                          and the
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                                                                                                                                                                                                                                                                                                                                                                                              Bohnert H.J.,
                                                                                 by
                                                                                                                                                                                               Heidelberg
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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ra Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Ra Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Ra Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Ra Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Ra James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Hunt S., Jagels K., Ra James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Churcher K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Ra Goliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Ra Ra Taylor R., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Starp S., Stevens K., Warper K., Warper S., Stevens K., Walsh S.V., Warren T., Whitehead S., Ra Weltfens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S., Ra Gabel C., Fuchs M., Filtzc C., Holzer E., Moestl D., Hilbert H., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Ra Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Ra Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Ra Bominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Ra Jaga R.R., Cuzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Ra Jaga R.R., Cuzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Ra Jaga R.R., Cuzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Ra Jaga R.R., Cuzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Ra Jaga R.R., Cuzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Ra Jaga R.R., Cuzado L., Benito J., Beni
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ACPM_SCHPO
Pfam; Pf0050; pp-binding; 1.
ProDom; PD000887; Acyl_carrier; 1.
TIGREAMS; TIGR00517; acyl_carrier; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; pS00012; ACPL DOMAIN; 1.
Hypothetical protein; Fatty acid biosynthesis; Phosphopantetheine; Mitochondrion; Transit peptide; Oxidoreductase.
TRANSIT 1 28
MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                             EMBL; 269380; CAA93348.1; -.
HSSP; P02901; lACP.
InterPro; IPR003231; Acyl_carrier.
InterPro; IPR003880; Ppantne_attach.
                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Putative acyl carrier protein, mitoche
ubiquinone oxidoreductase 9.6 kDa sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPAC4H3.09.
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                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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Matches 4
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Matches
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 Y998_RHIME
Q52966;
30-MAY-2000 (
30-MAY-2000 (
15-JUN-2002 (
Hypothetical
                                                                                                                                                                                                                                                        PROSITE; PS0002
Semen; Plasma;
DOMAIN 28
                                                                                                                                                                                                     DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                     HOMOLINY,

fibronectin.",

Biochem. J. 243:195-203(1987).

FIUNCTION: THE BSP-A PROTEINS FROM SEMINAL PLASMA EXHI-

FIUNCTION: THE BSP-A PROTEINS ON THE RELEASE OF GONADOTROPINS. THE EXACT FUNCTION OF THESE PROTEINS OF THESE PROTEINS.

GONADOTROPINS. THE EXACT FUNCTION OF THESE PROTEINS OF THESE PROTEINS.
                                                                                                                                                                                                                                                                         InterPro; IPRO00562; FN_Type_II.
Pfam; PF00040; fn2; 2
PRINTS; PR00013; FNTYPEII.
ProDom; PD000995; FN_Type_II; 2.
SMART; SM00059; FN2; 2
PROSITE; PS00023; FIBRONECTIN_2; 2.
                                                                                                                                                                                                                                                                                                                                       PIR; A29156; A29156.
HSSP; P02784; 1PDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87270621; PubMed=3606570; Sairam Seidah N.G., Manjunath P., Rochemont J., Sairam "Complete amino acid sequence of BSP-A3 from bov Homology to PDC-109 and to the collagen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1987 (Rel.
13-AUG-1987 (Rel.
01-OCT-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seminal plasma protein BSP-A3.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFP3_BOVIN
P04557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                            Similarity
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                                                                                                          57
                                                                                                                                                                                          28
-73
29
43
43
74
88
115 /
(Rel. 39,
(Rel. 39,
(Rel. 41,
l protein R
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69
112 AA;
                                                                                                                                                 100.0%;
llarity 100.0%;
Conservative 0
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                                                                                                                                                                                                    ; Glycoprotein; 1
28 166
28 165
73 115
115
29 53
29 53
43 66
74 100 1
                                                                                                                                                                                            AA,
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05, Created)
05, Last sequence up
34, Last annotation
                                                                                                                                                                                          13410
 Last sequence up, Last annotation R00998.
                                Created)
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FIBRONECTIN TYPE-II, I
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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Pred. No.
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Pred. No. 2.3
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                         34E0FA4B71A9FDE6 CRC64;
                                                                                                                                                 Mismatches
                     update)
                                                    116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                          2.4e+02;
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. 2.3e+02;
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                                                                                                                                                                     DB 1;
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from bovine sem:
-binding domain (
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                                                                                                                                                                   Length 115;
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CRC64;
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Best Local S
Matches 4
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P44181;
01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weldner S., Galibert F.; "Analysis of the Chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O.,
Kerlavage A.R., Bult C.J., Tomb J.-F.,
                                                                                                                                                                                                                                                                    HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL591785; CAC45570.1; -. Interpro; IPR005133; PhaG_MnhG_YufB. Interpro; IPR005133; PhaG_MnhG_YufB; I. Ffam; PF03334; PhaG_MnhG_YufB; 1. TIGR01300; CPA3_mnhG_phaG; 1. Hypothetical protein; Complete proteome. SEQUENCE 116 AA; 12373 MW; 16F4C117E81C4D10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95276304; PubMed=7756693; Keller M., Roxlau A., Weng W.M., Schmidt M., Quandt J., Niehaus K., Jording D., Arnold W., Puehler A.; Molecular analysis of the Rhizobium meliloti mucR gene regulating "Molecular analysis of the exopolysaccharides succinoglycan and biosynthesis of the exopolysaccharides succinoglycan and
                                                                                                                                                           Hypothetical HI1406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R00998 OR
Rhizobium
                                                                                                                            Bacteria;
                                                                                                                                           Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21396507; PubMed-11481430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        galactoglucan."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae;
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                                                                                                                                                                                                                                                                                                                                SLDA
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                         Proteobacteria;
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(Rel.
(Rel.
                                                                                                                                         influenzae.
                                                                                                                                                                    (Rel. 32, Last sequence up
(Rel. 41, Last annotation
protein HI1406.
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                    32,
41,
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                      Created)
                                                                                                                         gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 1;
Pred. No. 2.4e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schmidt M., Quandt J., Niehaus K.,
                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                    118
                                                                                                                                                                                      update
 Clayton R.A., Kirkness
Dougherty B.A., Merrick
                                                                                                                                                                                                                                                   ₽
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 116;
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RESULT 20
CHH4_PENMO
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Matches 4
          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Lieace,)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Crustacean hyperglycemic hormone 4 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                             "Five crustacean hyperglycemic family hormones of Penaeus monodon: complementary DNA sequence and identification in single sinus glands by electrospray ionization-Fourier transform mass spectrometry."; Mar. Biotechnol. 2:80-91(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHH4.
Penaeus monodon (Penoeid shrimp).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Eucarida; Decapoda; Dendrobranchiata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHH4_PENMO 
097386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 13
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Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "whole-genome random sequencing and assembly of Haemophilus influenzae {\rm Rd}\:. ";
                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10804243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U32820; AAC23056.1; -.
                                                                                                                                                                                                                                                                                                                                                   Wilson
                                                                                                                                                                                                                                                                                                                                                                   Davey M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                      rissuE=Eyestalk;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penaeoidea;
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                                                                                                                                                                                      BIOLECHMOL 2:80-91(2000).

FUNCTION: ABUNDANT HORMONE IN THE SINUS GLAND OF ISOPODS AND DECAPODS WHICH CONTROLS THE BLOOD SUGAR LEVEL. HAS A SECRETAGOGUE ACTION OVER THE AMYLASE RELEASED FROM THE MIDGUT GLAND. MAY ACT AS A STRESS HORMONE AND MAY BE INVOLVED IN THE CONTROL OF MOLTING ANT REPRODUCTION (BY SIMILARITY).
                                                                                                                                                         HORMONES
                                                                                                                                                                       SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HI1406;
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118 AA; 13
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13325 MW; C1CAF33E6CBB3452 CRC64;
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                                                                                                                                                                         THE ARTHROPOD
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Pred. No. 2.4e+02
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.S.M.,
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RESULT 21
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Best Local s
Matches 4
InterPro; IPR001063; Ribosomal_L22.
Pfam; PF00237; Ribosomal_L22; I.
ProDom; PD001032; Ribosomal_L22; I.
TIGRFAMs; TIGR01044; rPIV_bact; 1.
PROSITE; PS00464; RIBOSOMAL_L22; I.
Ribosomal protein; rRNA-binding; Complete proteome.
Ribosomal protein; rRNA-binding; Gomplete proteome.
SEQUENCE 122 AA; 13048 MW; 63E9285E51901523 CRC64;
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Q9ZJR8;
30-MAY-2000
                                                                                                                                                                              EMBL; AE001547; AAD06800.1;
HSSP; P48286; 1BXE.
                                                                                                                                                                                                                                            entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99120557; PubMed-9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doi Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50S ribosomal protein L22.
RPLV OR JHP1234.
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence comparison of two unrelated isolates of the gastric pathogen Helicobacter pylori.";
Nature 397:16-180(1999).
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16-OCT-2001
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PEPTIDE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THIS PROTEIN BINDS SPECIFICALLY TO 23S IS STIMULATED BY OTHER RIBOSOMAL PROTEINS, E.G., IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RE
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                                                                                                          InterPro; IPR001063; Ribosomal_L22.|
pfam; pF00237, Ribosomal_L22; 1.|
proDom; pD001032; Ribosomal_L22; 1.|
proDom; TIGR01044; rp1V_bact; 1.|
pROSITE; pS00464; RIBOSOMAL_L22; 1.|
pROSITE; pS00464; RIBOSOMAL_L22; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
sEQUENCE 122 AA; 13076 MW; C3F02854DFBB7895 CRC64;
                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatic the European Bioinformatics Institute. They use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-26695 / ATCC 700392;

MEDLINE-97394467; PubMed-9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klank H.-P., Gill S., Dougherty B.A.,

Relsochmann R.D., Ketchum K.A., Klank H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Nelson K., Quackenbush J., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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16-OCT-2001 (R
50S ribosomal
                                                                                                                                                                                                                       EMBL; AE000633; AAI
HSSP; P48286; 1BXE.
TIGR; HP1314; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 388:539-547(1997).

-i- FUNCTION: THIS PROTEIN BINDS SPECIFICALLY TO 23S RRNA; ITS BITS STIMULATED BY OTHER RIBOSOMAL PROTEINS, E.G., L4, L17, AND IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RECONSTITUTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                     Local Similarity
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RESULT
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A Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A de Nosa P.E., Roberto P.G., Poreira H.A. Jr., Pesquero J.B.,
A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A de Rosa V.E. Jr., de Sa R.G., Santesli R.V., Sawasaki H.E.,
A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silva A.C.R., Silvestri M.E.Z., Siqueira W.J., de Souza A.A.,
A da Silveira J.F., Silvestri M.E.Z., Siqueira W.J., de Souza A.A.,
A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A 2290 M.A., Zatz M., Meidanis J., Setubal J.C.;
The genome sequence of the plant pathogen Xylella fastidiosa.";
L. Nature 406:151-159(2000).

C. TEPD. IN SILVEIN SIL IS INVOLVED IN THE TRANSLATION INITIATION
                                         Matches
                                                                                                                      Pfam; PF00164; Ribosomal_S12; 1.
PRINTS; PR01034; RIBOSOMALS12.
PRODOM; PD000576; Ribosomal_S12; 1.
PTGRFAMS; TIGR00981; rpsL_bact; 1.
PROSITE; PS00055; RIBOSOMAL_S12; 1.
Ribosomal protecin; Complete protecome.
SEQUENCE 124 AA; 13695 MW; 50211B
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Q9PA88;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                      EMBL; AE004069; AAF85428.1; ALT_INIT. InterPro; IPR000230; Ribosomal_S12.
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                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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                                                           Local
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SIMILARITY: BELONGS TO THE S12P FAMILY OF RIBOSOMAL PROTEINS.
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                                                             Similarity
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                                         Conservative
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                                         0;
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                                                           Score 18; E
Pred. No. 2.
                                                                                                                          50211BD3A42C9FD1 CRC64;
                                         Mismatches
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                                                                                 DB 1;
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s 0;
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PDB; 2PLH; 03-APR-96. InterPro; IPR001010; Pfam; PF00321; plant_

PS00271;

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RESULT 24
THN1_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The amino acid sequence of purothionin A, to brewer's yeast from wheat."; Agric. Biol. Chem. 39:2269-2277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Endosperm;

MEDLINE=95125120; PubMed=7824649;

MEDLINE=95125120; PubMed=7824649;

Castagnaro A., Marana C., Carbonero P., Gau
"CDNA cloning and nucleotide sequences of a
thioning from hexaploid wheat endosperm.";

Plant Physiol. 106:1221-1222(1994).
                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Teeter M.M., Ma X.-Q., Rao U., Whitlow M.;
"Crystal structure of a protein-toxin alpha 1-purothionin
a comparison with predicted models.";
proteins 8:118-132(1990).
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[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Amino acid wheat.";
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                                                                               or send an email to license@isb-sib.ch).
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                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                    FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE PROTEINS IS NOT KNOWN.
                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
A01807;
                          x70666; CAA50004.1;
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VSWTA2
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onin A, a lethal toxic
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RESULT 25
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01-MAR-1989 (Rel. 1
01-MAR-1989 (Rel. 1
01-DEC-1992 (Rel. 7
                                                                                                 EMBL; D10879; BAA01679.1; -. EMBL; X14112; CAA32308.1; -. EMBL; M62932; AAA45829.1; -.
                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                 SEQUENCE
                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                             Al-Kobaisi M.F., Rixon F.J., McDougall I., Preston V.G., "The herpes simplex virus UL33 gene product is required assembly of full capsids.";
                                                                                                                                                                                                                                                                                                                                        McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., McNab B., Perry L.J., Scott J.E., Taylor P., "The complete DNA sequence of the long unique region i herpes simplex virus type 1.", Gen. Virol. 69:1531-1574(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphaherpesvirinae;
NCBI_TaxID=10299;
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                                                                                          F30085;
                                                           PF03581; Herpes_UL33; 1.
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                                                                           IPR005208; Herpes_UL33.
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                                                 130 AA;
    Conservative
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10, Last sequence update)
24, Last annotation update)
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Rixon F.J., McDo
                                             14437 MW;
             100.0%;
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  Score 18; DB
Pred. No. 2.7
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                                            >D: TEMPERATURE SENSITIVE.
D04CFDA7A3C585D3 CRC64;
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Pred. No.
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T GROUPS TOGETHER HSV-1 UL33,
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            2.7e+02;
                       DB 1;
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                     Length 130;
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RESULT 27
SFP1_BOVIN
ID SFP1_B
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     SFP1_BOVIN
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Hypothetical protein; Complete proteome.
CONFLICT 43 43 S -> L (IN REF.
                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                              EMBL; AE007157; AAK47854.1; TIGR; MT3516; -.
                                                                                                                                                                                                                                                                                                          EMBL; Z77165; CAB01015.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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Q50717;
Q1-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein Rv3408,
Hypothetical protein Rv3408.
Rv3408 OR MT3516 OR MTCY78.20C.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CDC 1551 / Oshkosh;
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                                                                                                                                                                Local Similarity
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   STANDARD;
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                                                                                                                                                                                                              14294 MW;
                                                                                                                                                             100.0%;
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                                                                                                                                                             Score 18; Pred. No.
 PRT;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Seminal plasma protein PDC-109 precursor (Sem
protein 109) (SVSP109) (BSP-Al and BSP-A2).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
                                                                                                  Constantine K.L.,
                                                                                                                                 STRUCTURE
                                                                                                                                                          Biochemistry
                                                                                                                                                                                                              STRUCTURE BY NMR OF 95-134.
MEDLINE-91129241; PubMed-1993183;
Constantine K.L., Ramesh V., Bany
                                                                                                                                                                                                                                                                        Gerwig G.L., Calvete J.J., Toepfer-Petersen E., Vliegenthart J.F.G.; "The Structure of the O-linked carbohydrate chain of bovine seminal plasma protein PDC-109 revised by H-NMR spectroscopy A correction."; FEBS Lett. 387:99-100(1996).
                                                                                                                                                                                                                                                                                                                               STRUCTURE OF CARBOHYDRATE ON THR-36. MEDLINE=96234019; PubMed=8654577;
                                                                                                                                                                                                                                                                                                                                                                          spermatozoa.";
FEBS Lett. 350
                                                                                                                                                                                                                                                                                                                                                                                                   seminal plasma and
                                                                                                                                                                                                                                                                                                                                                                                                                   O-linked to bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYDRATE-LINKAGE SITE THR-36.
MEDLINE-9435009; PubMed-8070564;
Calvete J.J. Raida M., Sanz L., Wempe F.,
Toepfer-Petersen E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-83256590; PubMed-6870895;
Esch F.S., Ling N.C., Boehlen P., Ying S.Y., Guillemin R.;
"Primary structure of PDC-109, a major protein constituent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Braeuer C.C., Klei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of the gene for the bovine secretory protein SVSP109.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
                                                         domain b.
                                                                                                               MEDLINE=92114067;
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                                                                                                                                                                                                    Llinas M.;
                                                                                                                                                                       Sequence-specific of bovine seminal
                                                                                                                                                                                                                                                                                                                                                                                                  Localization and structural characterization of an oligosaccharide linked to bovine PDC-109. Quantitation of the glycoprotein in eminal plasma and on the surface of ejaculated and capacitated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Cloning
                                                                        Refined
                                            MOL.
ain b. A collagen-binding type II domain.",

1. Biol. 23:281-298(1992).

FUNCTION: COULD ENHANCE THE FERTILIZING CAPACITY OF BULL

SPERMATOZOA UPON INTERACTION WITH HEPARIN-LIKE GLYCOSAMINOGLYCANS

PRESENT IN THE FEMALE GENITAL TRACT. EXHIBITS BOTH SIMULATORY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7:595-599(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                      solution structure and ligand-binding
. A collagen-binding type II domain.";
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(MAY-1994)
                                                                                                                              BY NMR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scheit K.H.;
and sequence analysis of a
the precursor of the major
                                                                                                                                                                                                                                                                                                                                                                          350:203-206(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-134, AND DISULFIDE
                                                                                                                                                       ecific 1H NMR assignments and structural characterization minal fluid protein PDC-109 domain b."; 30:1663-1672(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos.
                                                                                                  OF 95-134.
PubMed=1731074;
Madrid M., Bany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed-1932121;
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                                                                                                Banyai L.,
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                                                                                                  Trexler M.,
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Pecora; Bovoidea
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PIR; A31852; V
PIR; S18404; C
PIR; S45010; C
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000562; FN_Type_II.
Pfam; PF00040; fn2; 2.
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74
          1 SLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INHIBITORY ACTIONS ON THE RELEASE OF PITUITARY GONADOTRC SUBUNIT: HOMODIMER.
TISSUE SPECIFICITY: MAJOR COMPONENT OF SEMINAL PLASMA.
PTM: O-GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH MODIFIED WITH A SIALIC ACID RESIDUE (MACRO-AND/OR MICROHETEROGENEITY ACCOUNT FOR DIFFERENCES BETWEEN BSP-A
                                                                                                                                                                                                                                                                                                                                                                                                                              L; M22244; AAA30766.1; -.
L; X60495; CAAA3021.1; -.
L; X60496; CAAA3021.1; JOINED.
L; X60497; CAAA3021.1; JOINED.
L; X60498; CAAA3021.1; JOINED.
L; X60969; CAAA3021.1; JOINED.
L; X60960; -; NOT_ANNOTATED_CDS
L; X60960; -; NOT_ANNOTATED_CDS
L; X33621; CAA83915.1; -.
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SIMILARITY:
SLDA
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                                                                                                                                                                                                                                                                                           Plasma;
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                                       Similarity 4; Conser
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                                       100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                      FIBRONECTIN_2;
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                                                                                                                                                                                                                            SEMINAL PLASMA PROTEIN P FIBRONECTIN TYPE-II, A. FIBRONECTIN TYPE-II, B. O-LINKED (GALNAC. . .)./FTId=CAR_000071.
                                       0;
                                       Score 18; DE Pred. No. 2.8); Mismatches
                                                                                                                                                                                                                                                                                           Repeat;
                                                                               AD55FB8969B32224 CRC64;
                                                                                                                                                                                                                                                                                                      2
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                                                                                                                                                                                                                                                                                          Signal;
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                                               2.8e+02;
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RESULT 28
YHII_MYCLE S'
ID WHII_MYCLE S'
AC P49774; Q9R734;
DT 01-OCT-1996 (Rel

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RESULT 29
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P53902;
01-OCT-1996 (Rel. 3
01-OCT-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
14)Pothetical 14.8 k
YNL150W OR N1773.
                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0332; HISTRIAD.
PROSITE; PS00892; HIT; 1.
Hypothetical protein; Complete
SEQUENCE 134 AA; 14712 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001310; HIT. Pfam; PF01230; HIT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: BELONGS TO THE HIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P80912; 4RHN.
Leproma; ML2237; -.
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Barrell B.G.;
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Cole S.T., Eiglmeier K., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 SLDA 121
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Smith D.R., Robison K.;
Submitted (SEP-1994) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
Hypothetical HIT-like p
ML2237 OR MLCB5.04C OR
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NCBI_TaxID=1769;
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Z95151; CAB08415.1; -.
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4; Conser
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. 34, Last sequ
. 36, Last anno
                                                                   Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
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Last annotation updat
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protein ML2237.
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C1853F3ADF7239A7 CRC64;
                                                                                                                                                                     ation update)
RPC8-MFA2 intergenic region
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RESULT 30
THN2_WHEAT
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Best Local
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                                      Castagnaro A., Marana C., Carbonero P., Garcia-Olmedo F.;

"CDNA cloning and nucleotide sequences of alpha 1 and alpha 2
thionins from hexaploid wheat endosperm.";

Plant Physiol. 106:1221-1222(1994).

"PUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC REFECT AT THE
LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,

OF THESE PROTEINS IS NOT KNOWN.

"INSIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
                    This
                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence up
01-NOV-1995 (Rel. 32, Last annotation
                                                                                                                                                                  TISSUE=Endosperm;
MEDLINE=95125120; PubMed=7824649;
                                                                                                                                                                                                                                                 Triticum aestivum (Wheat).

Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                     Alpha-2-purothionin
THI1.2 OR PUR-B1.
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its councer. In modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                            P32032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                             THN2_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
DOMAIN 41 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A 43.5 kb segment of yeast chromosome XIV, which contains MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, prediadenosine deaminase gene and 14 new open reading frames."; Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 SLDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96287653; PubMed=8686380;
Nasr F., Becam A.-M., Herbert C. J.
"The sequence of 36.8 kb from the
24 complete open reading frames: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96109932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 104-135 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast 12:169-175(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SLDA 4
SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                  precursor.
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22EC1EC99F3DDD45 CRC64;
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left arm of chromosome XIV rev
contespond to new genes, one
the correspond to new genes, one
the human myotonic dystrophy
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a; Poales; Poaceae; Pooideae;
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frames.";
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    a collaboration -
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Best Local S
Matches 4
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THNB_WHEAT
P01543;
P01543;
21-JUL-1986
15-JUL-1998
15-JUL-1998
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Thionin;
                                                                                                                                                                          Ohtani S., Okada T., Kaga
"The amino acid sequence
to brewer's yeast from wh
Agric. Biol. Chem. 39:226
                                                                                                                                                                                                                                     SEQUENCE
Ohtani S.
                                                                                                                                                                                                                                                                                                               STRAIN-cv. Manitoba 3;
MEDLINE-78026451; PubMed-914810;
Ohtani S., Okada T., Yoshizumi H., Kaga
"Complete primary structures of two sub-
lethal protein for brewer's yeast from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X70665; CAA50003.1; -. PIR; S31695; S31695. HSSP; P01543; 1BHP. InterPro; IPR001010; Thionin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                              SEQUENCE OF 28-72.
MEDLINE-77046666; Pub
Mak A.S., Jones B.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purothionin THI1.3.
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                  X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
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| 133 SLDA 136
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                                                                                                                                                                                                                                                                                               thal protein for brewer's yeast Biochem. 82:753-767(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLDA 4
                                                         amino acid sequence of wheat J. Biochem. 54:835-842(1976).
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ted (JUN-1997) to
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Rao U.,
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(Rel. 36,
(Rel. 36,
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                                                                                                                                                                                                                                                        28-72
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                                                                                                                     PubMed=990986;
                                                                                                                                                                                              gruence of purothionin from wheat.";
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o the EMBL/GenBank/DDBJ databases
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ACIDIC PROTEIN.
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                                                                           beta-purothionin.";
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a; Poales; Poaceae; Pooideae;
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                                                                              RESULT 32
NXT1_CAEEL
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Acta Crystallogr. D 51:914-924(1995).
-i- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-20036817; PubMed-10567585;
Black B.E., Levesque L., Holaska J.M
"Identification of an NTF2-related f
regulates nuclear protein export.";
Mol. Cell. Biol. 19:8616-8624(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF004018; AAB71137.1; -. PIR; A01806; VSWTA1.
PDB; 1BHP; 15-MAR-96.
InterPro; IPR001219; Neurotoxii
InterPro; IPR001010; Thionin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9U757;
16-OCT-2001
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PRINTS; PR00284; TOXIN.
PROSITE: PS00271; THIONIN; 1.
Thionin; Plant toxin; Signal; 3D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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NXT1 OR Y71F9AM.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239
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Pred. No. 2.8e+02;
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tor that binds Ran-GTP an
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CO-92 / Biovar Orientalis;

MEDLINE-21470413; PubMed=11586360;

Parkhill J. Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague."

Nature 413:523-527(2001).
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P13662; IOUN.
WormPep; Y71F9AM.5; CE25780.
Interpro; IPR002075; NTF2.
Pfam; PF02136; NTF2; 1.
PROSITE; PS50177; NTF2_DOMAIN; 1.
Transport; Protein transport; mRNA transport; Nuclear protein.
DOMAIN 19 135 NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                      EMBL; AJ414155; CAC92416.1;
                                                                                                                                                                                                                                                                                                                                                   similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /BZC44;
/BZC44;
15-JUN-2002 (Rel. 41, Createu)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YERPE
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                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yersinia pestis
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SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute. The by non-profit institutions as long a by non-profit institutions as long a fifted and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF156960; AAD54945.1; AC024852; AAK66028.1;
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IPR000139;
l029; NusB;
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                BELONGS TO THE NUSB FAMILY.
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Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B99ABE3CA3479962 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                process (By
                                                                                                                                                                                                                                                        a collaboration -
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POC OC OC DIT
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HFAA_CAUCR
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PSB2_ECOLI
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Best Local Similarity
Matches 4; Conser
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                                                                                                                                                                     HFAA_CAUCR STANDARD; PRT; 147 AA.
P27342; 068957;
01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
H0-10fast attachment protein A (HfaA protein) (Hfa-A).
HFAA OR CC2628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989
01-MAR-1989
01-FEB-1991
                                                                   Caulobacter
                                                                                                 Bacteria; Proteobacteria; alpha
                                                                                                                                          Caulobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=89083490; PubMed=3205720; |

MEDLINE=80083490; PubMed=8008349; |

MEDLINE=8008349; |

MEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for psiB enhanced expression in plasmid R6-5.";
Nucleic Acids Res. 16:10669-10679(1988).
-i- FUNCTION: INHIBITION OF THE INDUCTION OF THE SOS PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dutreix M., Baeckman A., Celerier J., Bagdasarıan m.m., Summer S., Bailone A., Devoret R., Bagdasarıan M.; Bailone A., Summer Bailone B., Summer B., Summer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription termination; Con
SEQUENCE 138 AA; 15506 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 SLDA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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MW; 71A9A0307E6473A9 CRC64;
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                                                                                             subdivision; Caulobacter group;
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P39573;
01-FEB-1995
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CONFLICT
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STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed=11259647;
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STRAIN-AFCC 19089 / CB15;
MEDLINE-99138730; PubMed-9973336;
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"Analysis of a Caulobacter crescentus gene cluster involved attachment of the holdfast to the cell.";

J. Bacteriol. 174:687-694(1992).
         30S ribosomal protein S12P RPS12P OR RPS12 OR RPS12AB
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Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-i- FUNCTION: INVOLVED IN ATTACHMENT OF THE HOLDFAST TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 181:1118-1125(1999)
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S.MARCESCENS SMFG C-TERMINI.
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147 AA;
solfataricus
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09B10FE5DFDF436F CRC64;
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M., White O.,
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Matches 4
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SEQUENCE
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EMBL; AE006659; AAK40562.1; ALT_INIT.
InterPro; IPR000230; Ribosomal_S12.
Pfam; PF00164; Ribosomal_S12; 1.
ProDom; PD000576; Ribosomal_S12; 1.
TICRFAMS; TIGR00982; S23_S12_E_A; 1.
PROSITE; PS00055; RIBOSOMAL_S12; 1.
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                         Sulfolobus tokodaii.
Archaea; Crenarchaeota;
                                                                RPS12P OR ST0272.
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MEDLINE-21332296; PubMed-11427726;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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Pred. No. 3.1e+02;
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RESULT 38
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Collins J.H.;
                                                                                                                                                                   TISSUE-Abdominal flexor muscle;
MEDLINE-92027802; PubMed-1929438;
Garone L., Thelbert J.L., Miegel A.,
                                                                                                                                                                                                                                                             Homarus americanus (American lobster).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Astacidea; Nephropoidea; Nephropidae; Homarus.
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Pfam; PF00164; Ribosomal_S12; 1.
ProDom; PD000075; Ribosomal_S12; 1.
TIGRFAMs; TIGR00982; S23_S12_E_A; 1.
PROSITE; PS00055; RIBOSOMAL_S12; 1.
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                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                             NCBI_TaxID=6706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
-I- FUNCTION: Protein S12 is involved in the translation initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome. SEQUENCE 147 AA; 16336 MW; 5BC87E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP000982; BAB65239.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=JCM 10545 / 7;
MEDLINE=21456156; PubMed=11572479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 SLDA 136
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SIMILARITY: BELONGS TO THE S12P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                          Nephropoidea; Nephropidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0
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Pred. No. 3
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                                                                                                                                                                    Maeda
                                                                                                                                                                                                                                                                                                                                                                                       150 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1e+02;
s 0;
                                                                                                                                                                Y., Murphy C.,
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RESULT 39
MRAZ_PSEAE
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Matches 4
                                                      TIGRFAMS; TIGR0024; Complete proteome. SEQUENCE 151 AA;
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMMI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 15692 / PAO1;

MEDLINB-2043737; PubMed-10984043;

Stover C.K. Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                        EMBL; AE004856; AAG07809.1; -.
                                                                                                                                                                                                                                                                        "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                  Pfam; PF02381; UPF0040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA_BIND
SEQUENCE
                                                                                                                 InterPro;
                                                                                                                                                                                                                                                              -! SIMILARITY: BELONGS TO THE MRAZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRAZ OR PA4421.
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CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas
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MUSCLE protein; Calcium-binding; Repeat; Acetylation.

ACETYLATION (BY SIMILARITY)

ACETYLATION (BY SIMILARITY)

ACETYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00036; efhand; 4. ProDom; PD000012; EF-hand; 2. SMART; SM00054; EFh; 4.
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||||
3 SLDA 6
                  Similarity
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                                                                                    TIGR00242;
                                                                                                              IPR003444; UPF0040.
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23
56
96
132
150 AA;
     Conservative
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67 E
107 A
143 E
; 16951 MW;
                                                         17111 MW;
               100.0%;
                                                                                    TIGR00242;
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    0;
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            Score 18; DB 1;
Pred. No. 3.2e+02;
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EF-HAND 2 (PROBABLE).
ANCESTRAL CALCIUM SITE 3
EF-HAND 4 (PROBABLE).
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Pred. No.
                                                       2E653E29E113216B CRC64;
  Mismatches
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                           Length 151;
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Gaps
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OS Rh
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Best Local
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P55518;
01-NOV-1997
01-NOV-1997
15-JUN-2002
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P11524;
01-OCT-1989
                                                                                                                                                                                                   LT 41
RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Organization and nucleotide sequence of the subunits A, B and C of the DNA-dependent RNA archaebacterium Sulfolobus acidocaldarius. *, Nucleic Acids Res. 17:4517-4534(1989).

-I- FUNCTION: PROTEIN S12 IS INVOLVED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00164; Ribosomal_S12; 1.
ProDom; PD000576; Ribosomal_S12; 1.
TIGRRAMS; TIGR00982; S23_S12_E_A; 1.
PROSITE; PS00055; RIBOSOMAL_S12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X14818; CAA32929.1; ALT_INIT. PIR; S04721; R3UC12. InterPro; IPR000230; Ribosomal_S12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 33909 / NCIB 11770 / DSM MEDLINE-89315197; PubMed-2501756;
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                                                                  Plasmid sym pNGR234a.
Bacteria; Proteobacteria;
                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Puehler G., Lottspeich F., Zillig W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995
30-MAY-2000
 SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
                                                      Rhizobiaceae; Rhizobium.
                                                                                             Rhizobium sp.
                                                                                                                                                                                                                                                            133
                                                                                                                                                                                                                                                                                                                                                                              Ribosomal protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPS12P OR RPS12
                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                    1 SLDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal protein
                                                                                                                                                                                                                                                          SLDA 136
                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
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(Rel. 35,
(Rel. 41,
11 17.3 kDa
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                                                                                             (strain NGR234).
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39,
                                                                                                                                                                                                                                                                                                                                                                 16570 MW;
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Last annotation update)
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                                                                  alpha
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                                                                                                                                                                                                                                                                                                                       Score 18; DB 1;
Pred. No. 3.2e+02;
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                 3867AE02D161491F CRC64;
                                                                                                                                                                                                                                                                                                             Mismatches
                                                                   subdivision;
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                                                                   Rhizobiaceae
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                                                                                                                                                                                                                                                                                                                                      Length 151;
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[nterPro;

Pro; IPR002750; PF01890; CbiG;

CbiG.

biosynthesis; Porphyrin biosynthesis.
154 AA; 15487 MW; 197D77DC4CE20BAE CRC64;

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RESULT 42
COBE_PSEDE
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Best Local :
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P21635;
01-MAY-1991
01-MAY-1991
01-JUL-1993
                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                  Crouzet J., Cauchois L., Blanche F., Debussche L., Thibaut D., Rouyez M.-C., Rigault S., Mayaux J.-F., Cameron B.; "Nucleotide sequence of a Pseudomonas denitrificans 5.4-kilobase DNI fragment containing five cob genes and identification of structural genes encoding S-adenosyl-L-methionine: uroporphyrinogen III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401(1997).
-!- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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SMART; SM00448; REC;
                                                          EMBL; M59236; AAA25772.1; -. PIR; A36144; A36144.
                                                                                                                                                                                                                                                      methyltransferase and cobyrinic acid a,c-diamide synthase J. Bacteriol. 172:5968-5979(1990).
                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SC510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CobE protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           eudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 SLDA 115
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                                                                                                                                                                                                                         TO COBYRINIC ACID.
                                                                                                                                                                                                                                        PATHWAY: COBALAMIN BIOSYNTHESIS; TRANSFORMATION OF PRECORRIN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 18, Created)
(Rel. 18, Last seq
(Rel. 26, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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; F8B42BCF7845E03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 1;
Pred. No. 3.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            jht. It is produced through a c
Bioinformatics and the EMBL
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                                                                                                                                                                                             collaboration
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VATL_HELVI
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Best Local :
         BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L16884; AAC37176.1; -.
InterPro; IPR002379; ATPase_Csub.
InterPro; IPR000245; Vac_ATPsynt_Csub.
Pfam; PF00137; ATP-synt_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and LOI communications requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996
01-OCT-1996
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pietrantonio P.V., Gill S.S.;
"Sequence of a 17 kDa vacuolar H(+)-ATPase proteolipid subunit from insect midgut and Malpighian tubules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ditrysia;
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Eukaryota; Metazoa; Arthropoda; Mar
Insecta; Pterygota; Neoptera; Endor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vacuolar
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P55277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AS A HEXAMER THAT FORMS THE PROTON CONDUCTING PORE).
SUBCELLAULAR LOCATION: Integral membrane protein. Vacuolar MISCELLAUBOUS: THIS SUBUNIT BINDS DICYCLHEXYLCARBODIIMIDE (DCI WHICH INHIBITS THE ATPASE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H(+)(Out).

SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON POR COMPLEX (MAIN COMPONENT: THE PROTECULIPID PROTEIN; WHICH IS PREDEDLED TO THE PROTECULIPID PROTEIN; WHICH IS PROTECULIPID PROTECULIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE INTEGRAL VO COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLDA 58
                                                                                                                                                                                                                                                                                                                                                                                                              PR00122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                        TIGRO1100; V_ATP_synt_C; 1.
; Hydrogen ion transport; ATP_synthesis; Transmembrane.
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153
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nilarity 100.
Conservative
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
P synthase 16 kDa proteolipid subu
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52
73
92
114
126
152
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rthropoda; Mandibulata; Pan-

eoptera; Endopterygota; Lep-

Noctuidae; Heliothinae; He
         MW;
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DICYCLOHEXYLCARBODIIMIDE E8DB1065B896E4B5 CRC64;
                                                                                                                  POTENTIAL.
CYTOPLASMIC
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Pred. No. 3.2e+02;
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                                                                                            POTENTIAL.
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                                                               LUMENAL (POTENTIAL)
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                                                                                                                                                                                                                                              CYTOPLASMIC
                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                           (POTENTIAL).
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                         (POTENTIAL).
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RISB_MYCTU
ID RISB_MA
AC P71685
DT 01-NOV
DT 16-OCT
DT 15-JUN
DE 6,7-d1
DE (Lumaz
GN RIBH C
OS Mycoba
OC Bacter
OC Actinc
OX NCBLT
RN [1]
RP SEQUEN
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Best Local
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Best Local :
                                                                                                                        RISB_MYCTU
P71685;
01-NOV-1997
16-OCT-2001
15-JUN-2002
                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.
(Lumazine synthase) (Riboflavin synthase beta
RIBH OR RV1416 OR MT1459 OR MTCY21B4.34.
                                                     (Lumazine synthase) (Ribofl
RIBH OR KV1416 OR MT1459 OR
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P16792;
01-AUG-1990
01-AUG-1990
01-FEB-1991
                          Actinomycetales; NCBI_TaxID=1773;
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03581; Herpes_UL33;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X17403; CAA35410.1; -. PIR; S09814; S09814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of the protein-coding content cytomegalovirus strain AD169.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-coding content of the sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _HCMVA
UL51_HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=90269039; PubMed=2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical UL51.
                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S09814; S09814.
InterPro; IPR005208; Herpes_UL33.
                                                                                                                                                                                                                                                       92 SLDA 95
                                                                                                                                                                                                                                                                                 1 SLDA 4
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4; Conservative
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157 AA; ]
                                                                                                                                                                                                                                                                                                            Conservative
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(Rel. 15, Last sequence up
(Rel. 17, Last annotation)
l protein UL51.
                                                                                                                                                                                 STANDARD;
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                                        Corynebacterineae;
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                                                                                                                                                     Created)
                                  Actinobacteria (class); Actcterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                  MW;
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                                                                                                                                                                                                                                                                                                                        Score 18; I
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Pred: No. 3.3e+02;
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REMBL; AE007016; AAK45724.1; -.

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RIGR; MT1459; -.

RIGR; MT1459; -.

RIUDATCULIST; RV1416; -.

DMRL_Synthase: 1.

RIUDATCULIST; DMRL_Synthase: 1.

RPCDDom; PD003664; DMRL_Synthase; 1.

RPCDDom; PD003664; DMRL_Synthase; 1.

RPCDDom; PD003664; DMRL_Synthase; 1.

RTIGREAMS; TIGRO0114; TibH; 1.

RTIGREAMS; TIGRO0114; TibH; 1.

RRUGHIAVIN bioSynthesis; Transferase; Complete proteome.

MRIDGILAVIN bioSynthesis; Transferase; Complete proteome.

SEQUENCE 160 AA; 16370 MW; 20E837C273312E83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).

-- CAPALYTIC ACTIVITY: 26,7-dimethyl-8-lu-pribityl-lumazine -- riboflavin +4-(1-D-ribityl-amino)-5-amino-2,6-dihydroxypyrimidine.

-- PATHWAY: Riboflavin biosynthesis; last step.

-- SIMILARITY: BELONGS TO THE DMRL SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98295987; pubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

KOlonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

Belchat M., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                       Chistoserdova L., Lidstrom M.;
"Cloning of a hydroxypyruvate reductase gene from Methylobacterium
"Cloning of a hydroxypyruvate reductase gene from Methylobacterium
extorquens AMJ, mutagenesis of the gene.";
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; M/4226; AAA25377.1;
Oxidoreductase; Pyruvate.

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Andreoni F., Ruzzo A.,
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"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."

Nature 409:529-533(2001).

EMBL, AE005559; ARG59475.1; -
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MEDLINE=21074935; PubMed=11206551;
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Pred. No. 4.1
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21166612AB82447B CRC64;
                PRT;
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thes 0;
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Best Local :
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Ben-Arie N., McCall &
Zoghbi H.Y.;
"Evolutt"
                                                                                                                                                                                                                                     Q94791; PRELIMINARY; Q94791; 01-FEB-1997 (TIEMBLIEGL. 0 01-FEB-1997 (TIEMBLIEGL. C 01-MAR 2002 (TIEMBLIEGL. 2
                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                         "Evolutionary conservation of sequence and expression of protein Atonal suggests a conserved role in neurogenesis. Hum. Mol. Genet. 5:1207-1216(1996).

EMBL; U61152; AAB41307.1;
                                                                                                                                                                                        Eukaryota; Metazoa; Arthropo
Pterygota; Neoptera; Endopte
Cucujiformia; Tenebrionidae;
                                                                                                                                                                                                 Tribolium castaneum
Eukaryota; Metazoa;
Pterygota; Neoptera;
                                                                                      SMART;
                                                                                            InterPro; IPRO(
Pfam; PFO0010;
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STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Hypothetical protein zl1
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26
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29
                                                                                          IPR001092; HLH_basic.
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                              Conservative
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                                                             5263 MW;
                                                                                                                                                  Α.Ε.,
                                                                                                                                                                                    (Red flour beetle).
Arthropoda; Tracheata; Hexapoda; Insecta;
Endopterygota; Coleoptera; Polyphaga;
rionidae; Tribolium.
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Q8SPU2;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
        Q941Y6;
Q941Y6;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
P0431G06.24
P0431G06.24
                                                                                                                                                                                                                                                                                                                                           Q9NMC6
Q9NMC6;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2000
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Murphy L., Quail M., Harris
Submitted (JUL-2000) to the
EMBL; AL160493; CAB97784.1;
NON_TER 51 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Cercopithe
Cercopithecinae; Macaca.
NCBI_TaxID=9544;
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Local Similarity 100.0%;
hes 4; Conservative (
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      (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
protein (B1139B11.2 protein).
OR B1139B11.2.
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(TrEMBLrel. 15, Last sequence up)
(TrEMBLrel. 15, Last annotation
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(Rice),
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EMBL/GenBank/DDBJ
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Pred. No. 5.
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5.2e+02;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21595285; PubMed-11759840;
MEDLINE-21595285; PubMed-11759840;
MEDLINE-21595285; PubMed-11759840;
Manaka T., Nakamura Y., Wolk C.P., Kuritz T., Sasan Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasan Kaneko T., Nakamura Y., Kohara M., Matsumoto M., Matsuno A., Matsuno A., Matsuno A., Matsuno A., Matsuno A., Shimpo S., Sugimoto M., Takazawa M.,
                                                                                                                                                                                                                                                                                                                    Q8YL68;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                        Plasmid;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica.cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBL_TaxID-4530, 39947;
[1]
                                                                                                           "Complete genomic sequence of the filamentous cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
EMBL; AP003600; BAB78151.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOY-2001) to the EMBL; AP003683; BAB64712.1; EMBL; AP004368; BAB90774.1; SEQUENCE 52 AA; 6048 MW;
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
clone:B1139B11.";
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:P0431G06.";
                                                                                                                                                                                                                                                            Anabaena sp. (strain PCC 7120).
Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostoc
                                                                                                                                                                                                                                                                                              Hypothetical protein ASR7067.
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Hypothetical protein; Complete proteome.
53 AA; 5639 MW; 3D75D4AA82284175 CRC
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(GA3) genomic
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Q9Z775;
01-MAY-1999
01-MAY-1999
                                                                      "Genomic sequence compreumoniae from Japan Submitted (JAN-2000)
                                                                                                                              STRAIN=J138;
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                            MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CPn0831
CPN0831 OR CPJ0831 OR CPJ0839.
                MEDLINE=20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C.,
                                                                                                                                                                   Submitted
                                                                                                                                                                                Hirakawa H.,
                                                                                                                                                                                          STRAIN-J138;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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Hypothetical protein; Complete proteome.
SEQUENCE 55 AA; 6406 MW; B7CE6B7FEFDAD6E2 CRC64;
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01-MAR-2002
01-MAR-2002
Putative rib
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                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=83558;
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Yersinia pestis.
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MEDLINE-21470413; PubMed-11586360;
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 Brunham R.C., Shen C
Hickey E.K., Peterson
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5 AA; 6406 MW; B7CE6B7FEFDAD6E2 CRC64;
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the EMBL/GenBank/DDBJ databases.
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Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F.
Shiba T., Ishi K., Hattori M., Kuhara S., Nakazawa T.,
Shiba T., Ishi K., Hattori M., Kuhara S., Nakazawa T.,
Comparison of whole genome sequences of Chiamydia pnet
from Japan and CWL029 from USA.";
LNucleic Acids Res. 28:2311-2314(2000).

EMBL; AE001663; AAD18968.1; -.
EMBL; AE002541; BAA88649.1; -.
EMBL; AE002541; BAA88649.1; -.
EMBL; AE002541; BAA888649.1; -.
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Q9K1Z5;
01-OCT-2000
01-OCT-2000
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  Q9ZI54
                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequences of Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20150255; PubMed=10684935; | Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hokey E.K., Peterson J., Utterback T., Berry K., B Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodso Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae (Cl
Bacteria; Chlamydiales;
NCBI_TaxID=83558;
                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 62 AA; 6840 MW;
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Eisen J., Fraser C.M
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Eisen J.,
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Nucleic Acids Res.
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Fraser C.M.;
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Nelson W., DeBoy R., Kolonay
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6 AA; 6344 MW; 0!
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AAF38560.1; -.
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Salzberg S.L.,
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EMBL; AF100302;
HSSP; P49172; 10
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092431; O1-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                      Plasmid.
SEQUENCE
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Nahy, a catabolic plasmid-encoded Pseudomonas putida to the aromatic J. Bacteriol. 181:3310-3316(1999).
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Pfam; PP01361; Tautomerase; 1.
ProDom; PD019232; Tautomerase;
TIGRFAMs; TIGR00013; taut; 1.
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Gene 245:65-74(2000).
EMBL; AF039534; AA002155.1;
HSSP; Q01468; IBJP.
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Pfam; PF01361; Tautomerase; 1.
ProDom; PD019232; Tautomerase;
TIGRFAMs; TIGR00013; taut; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99255564; PubMed-10322041;
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Last annotation update)
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Pred. No.
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                                                                                    Pred. No.
                                                                                                            Score 18;
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hydrocarbon naphthalene.";
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Q9R9T3;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
                                                                                                                                                                                                                                               Wessler H.G., Hares D.R., Poulter M.D., Voss J.A Baker R.F., Azadpour E.E., Luo X., Benjamin R.C. "Sequence of the lower (meta-cleavage) xyl opero putida TOL plasmid pDK1 ";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ da EMBL; AF134348; AAL83667.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Beilen J.B., Roethlisberger M., Witholt B.; "Organization of the Pseudomonas putida (oleovorans) GPol and Pseudomonas putida Pl alkane oxidation genes."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ249793; CAB66148.1; -.
HSSP; P49172; 10TF.
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-PAW630;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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ProDom; PD019232; Tautomerase;
TIGRRAMS; TIGR00013; taut; 1.
SEQUENCE 63 AA; 6996 MW; AJ
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                                                                                                            7e+02;
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Best Local :
                                                                Submitted (JAN-1999) to the EMBL/GenBank/DDBJ EMBL; AF123349; AAD30982.1; -. HSSP; P25685; 1HDJ. InterPro; IPR001623; DnaJ_N. InterPro; IPR003095; Hsp_DnaJ. Pfam; PF00226; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                  Mycobacterium xenopi.
Mycobacteria; Actinobacteria; Actinobacteridae
Bacteria; Firmicutes; Actinobacterineae; Mycobacteriaceae;
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2002 (TrEMBLrel. 20,
                         PRINTS; PR00625; DNAJPROTEIN SMART; SM00271; DnaJ; 1.
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NCBI_TaxID=1789;
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MEDLING=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
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Q9SJH4;
     PROSITE;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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7.2e+02;
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Q9TU12;
01-MAY-2000
01-MAY-2000
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Uroplakin 3
                                                                          NON_TER
                                                         SEQUENCE
                                                                                                           STRAIN=NEW ZEALAND WHITE; TISSUE-BLADDER Cho S.K., Kwon D.N., Chu H.J., Kim J.H.; "Cloning of rabbit uroplakin III cDNA."; Submitted (AUG-1999) to the EMBL/GenBank EMBL; AF178938; AAD55729.1; -.
                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata; Craniata;
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Miller S.
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Mol. Microbiol. 18:479-490(1995).
EMBL; U30491; AAC43549.1; -...
NON_TER 65 65
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SEQUENCE
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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MEDLINE=96342378; PubMed=8748032; ,
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Bacteria; Proteobacteria;
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01-MAY-2000
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006571;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uroplakin 3 (Fragment).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartioda
NCBI_TaxID=9823;
                       SEQUENCE FROM N.A. STRAIN-CDC 1551 / OSHKOSH; Fleischmann R.D., Alland D.,
                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv1119c.
RV1119C OR MT1151 OR MTCY-2G8.08C.
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KWON D. N., Chu H.J., Cho S.K., Kim J
"Cloning of pig urophakin III cDNA."
Submitted (AUG-1999) to the EMBL/Genl
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; My
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 n J., DeBoy R., Dodson R., Gwinn J.F., Nelson W.C., Umayam L.A.,
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Last annotation updat
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           Eisen
un R., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286DF9159818E36A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 6;
Pred. No. 7.4e+02;
Mismatches 0;
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actyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                          J.A.,
                                                                                                                                                                                                                                                                             Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BLADDER UROTHELIUM;
.H.;
                                                                                                                                                                                                                                                                                       Actinobacteridae;
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M., Haft D., Hi, Ermolaeva M., S
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Sus.
             Hickey
                                                                                                                                                                                                                                                                             Mycobacterium
 Salzberg S.L.,
                          White
             E .
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SEQUENCE FROM N.A.

MEDLINE-99185141; PubMed-10085157;

COON S.L., Begay V., Deurloo D., Falcon
"Two arylalkylamine N-acetyltransferase
synthesis in fish.";
J. Biol. Chem. 274:9076-9082(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9MBV1;
                                                                                                                                                                                                                                    Q9PWK4:
01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequer
01-MAR 2002 (TrEMBLrel. 20, Last annote
Arylalkylamine N-acetyltransferase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole genome comparison laboratory strains."; Submitted (APR-2001) to EMBL; Z95585; CAB09051.1
                                                                                                                                              Eukaryota; Metazoa;
Actinopterygii; Neop
Esocidae; Esox.
                                                                                                                                                                                                                                                                                                                              Q9PWK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF133308; AAF43267.1; SEQUENCE 67 AA; 7586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21359315; PubMed=11466276;
Mukhopadhyay A.K., Chakraborty S., Takeda Y.,
Mukhopadhyay A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Hypothetical protein;
                                                                                                                                                                                                                         AANAT1
                                                                                                                                                                                                    Esox lucius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repressor-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssDNA viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delcher A.,
                                                                                                                                                                                                                                                                                                                                                                  24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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66 AA; 692
                                                                                                                                                                                   (Northern pike).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Utterback T., Weidman
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                               Neopterygii;
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6929 MW; 582B7A7D3C58CF10 CRC64;
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19,
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                                                                                                                                                                 : Craniata;
Teleostei;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
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                                                          Klein
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and C
                                         mediate melatonin
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Q95Y38
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Best Local :
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007227; OTEMBLE 04, C.
01-JUL-1997 (TREMBLE 04, L.
01-JUL-1997 (TREMBLE 04, L.
01-MAR-2002 (TREMBLE 20, L.
Hypothetical protein RV0300.
RV0300 OR MTCY63.05.
                                                                                           O95Y38, PRELIMINARY; PRT; 74 AA.
Q95Y38; O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Y77EIIA.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Cole S.Y., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                    Caenorhabditis elegans.
               Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 296800; CAB09591.1; -.
TubercuList; Rv0300; -.
InterPro; IPR002145; CopG_HTH_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome. SEQUENCE 73 AA; 8088 MW; 379D16E6EA7D7979 CRC64;
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NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; My
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HSSP; Q29495; ICJW.
ACYLTIANSFERASE; Transferase.
NON_TER 1 1 1
NON_TER 68 68
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                                        Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7711 MW;
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04, Last sequence update)
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                    Caenorhabditis
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Pred. No. 8.3e+02;
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Pred. No.
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EMBL; AJ293568;
SEQUENCE 74 A
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Q9DHK2;
Q1-MAR-2001
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01-DEC-2001
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Yaba-like
                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21176366; Pui
Lee H.J., Essani K.,
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                Lee H.J., Essani K., Smith G.L.;
"The genome sequence of Yaba-like disease virus, a
Virology 281:170-192(2001).
                                                                                                                                                                         Submitted
                                                                                                                                                                                                                         Yaba-like disease virus
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
74 AA; 8307 MW;
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Submitted (NOV-2001) to the
EMBL; AC024214; AAK67241.1;
                                                                                            Lee H.J.;
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STRAIN=BRISTOL N2;
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MEDLINE=99069613; PubMed=9851916;
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K., Smith G.L.;
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                               Pred. No. 8.4e+02; Mismatches 0;
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Genomic DNA,
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Q41970;
Q41970;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 19, Last annotation update)
ADP, ATP carrier protein (Fragment).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q53417;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAY-2000
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Desprez T., Amselem J., Chiapello H., Rouze P., Caboche M.,
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; Z18781; CAA79257.1; -.
InterPro; IRR001993; Mitoch_Carrier.
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Mol. Plant Microbe Interact. 7:173-180(1994).
EMBL; S70736; AAB31118.2; -.
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MEDLINE-94281668; PubMed-8012039;
Dockendorff T.C., Sharma A.J., Stacey
"Identification and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID-375;
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chromosome 3, BAC clone:F21A17.
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Pred. No. 8.5e+02;
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Q9KAKO;
01-OCT-2000
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                                                                                                                                                        "Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison wit Nucleic Acids Res. 28:4317-4331(2000).
EMBL; APO01515; BAB06006.1; -.
Complete proteome.
SEQUENCE 76 AA; 8916 MW; 6028CDFC766C6307
                                                                                                                                                                                                              STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y.,
Tuji F., Hirama C., Nakamura Y., Og
Horikoshi K.;
                                                                                                                                                                                                                                                                                               Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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Submitted (NOV-1999)
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O81534; O1-NOV-1998 (TIEMBLIEL. 08,
O1-NOV-1998 (TIEMBLIEL. 08,
O1-JUN-2002 (TIEMBLIEL. 21,
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Q47775;
01-NOV-1996
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                 Saccharum officinarum (Sugarcane).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Panicoideae; Andropogoneae; Saccharum.
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        NCBI_TaxID=4547
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EMBL; D78257; BAA11326.1;
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J. Bacteriol. 183:1405-1412(2001).
EMBL; AF322013; AA060986.1;
SEQUENCE 78 AA; 8994 MW; 8AA5AAF174C86355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
Bradyrhizobium group; Brad
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NCBI_TaxID=1351;
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Q92KC9;
Q1-DEC-2001
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                                                         Q42264 PRELIMINARY; PRT; 82 AA. Q42264; Q12264; Q1.NOV-1996 (TrEMBLrel. 01, Created), 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Carrier protein (Fragment). Arabidopsis thaliana (Mouse-ear cress).
                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                      Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591787; CAC46175.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 80 AA; 9461 MW; 7C02CD5F7830B99D CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein R01596, R801596 OR SMC01197.
           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-1021;
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"Sugarcane resistance to Striga hermonthica.";
"Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF09174; AAC27797.1;
InterPro; IPR001099; N-C_synthase. |
Pfam; PF00195; Chal_stil_synt; 1.
ProDom; PD000453; N-C_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21396507; PubMed-11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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bred. No. 9.1e+02;
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Q9NMB4;
Q1-OCT-2000
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Q1-JUN-2002
                                                                                                                                                                                          Chalcone synthase (Fragment).
Fragaria vesca subsp. bracteata.
Fragaria vesca subsp. bracteata.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
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Desprez T., Amselem J., Chiapello H., Caboche
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ
EMBL; Z33799; CAA83932.1; -.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 1.
              Deng C., Davis T.;

Molecular identification of the yell diploid strawberry: a candidate gene Theor. Appl. Genet. 0:0-0(2001).

EMBL; AY017485; AAK33142.1; ...
                                                                                                                                                                                                                                                                                                       094IT9:
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy L., Quail M., Harris Submitted (JUL-2000) to the EMBL; AL160493; CAB97796.1;
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Eukaryota; Eugle
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LM26.178.
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NCBI_TaxID=5664;
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STRAIN=CV. COLUMBIA;
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STRAIN-950Al; Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.; Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.; "Identification of Mycobacterium avium DNA Sequences the Exported Proteins by Using phoA Gene Fusions."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF143401; AAF74995.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diploid strawberry: a candidate gene Theor. Appl. Genet. 0:0-0(2001). EMBL; Av017477; AAK33134.1; ... InterPro: IPR001099; N-C_synthase. pfam; PF00195; Chal_stil_synt; 1. ProDom; PD000453; N-C_synthase; 1.
                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria;
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01-OCT-2000 (TREMBLRel. 15, Last sequence update)
01-OCT-2000 (TREMBLRel. 15, Last annotation updat
Exported protein 996A160 (Fragment).
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ProDom; PD000453; N-C_synthase;
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                                                                                                                                                          SEQUENCE FROM
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NCBI_TaxID=1764;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                          N.A.
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Pred. No.
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Pred. No. 9.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FE2EC3F6AE0C1239 CRC64;
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9.6e+02;
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udicots; Rosidae;
                                                                                         that
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                   Q93EF2;
Q93EF2;
01-DEC-2001 (
01-DEC-2001 (
01-DEC-2001 (
                                                                                        "Ge Z., Feng Y., Fox J.G.;
"Helicobacter hepaticus genome: construction of an ordered cosmid library and sequence analysis of the selected genomic regions."; submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF358712; AAL16703.1; -.
         SEQUENCE
                                                                                                                                                                                                            STRAIN=3B1;
                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Hypothetical 10.3 kDa protein (Fragment).
Helicobacter hepaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Veronesi C., Labrousse P., Thalouarn P.;
"Histological, physiological and molecular aspects of su
resistance to Orobanche cumana.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF074401; AAC26132.1; -.
InterPro. IPR001099; N-C_synthase.
Pfam; PF00195; Chal_stil_synt; 1.
ProDom; PD000453; N-C_synthase; 1.
NON_TER 85 85
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O81399; O1-NOV-1998 (TREMBLrel. 08, Created)
O1-NOV-1998 (TREMBLrel. 08, Last sequence update)
O1-JUN-2002 (TREMBLrel. 21, Last annotation updat
                           NON_TER
                                                                   Hypothetical protein.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  Helicobacter
                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Orobanchaceae; Orobanche.
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SEQUENCE
                                                                                                                                                                                                                                                                           NCBI_TaxID=32025;
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les 4; Conservative
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    MW;
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                                                                                                                                                                                                                                                                                                                epsilon subdivision; Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB LU;
Pred. No. 9.8e+02;
Pred. No. 9.8e+02;
406A612F41A3EFD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB
Pred. No. 9.8
0; Mismatches
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MEDLINE-20504483; PubMed-11016950;

X MEDLINE-20504483; PubMed-11016950;

RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

RT "Genome sequence of Halbbacterium species NRC-1.";

RT "Genome sequence of Halbbacterium species NRC-1.";

RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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Best Local
EQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21608550; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo

Thang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry

Thang S., Yoo H., Tao Y., Biddle P., Hendrick C., Zhao Z.-Y., Dolan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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Q8UJ19;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
Hypothetical protein Atu0119.
                                                                                                                                                                                                     Agrobacterium tumefaciens
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                               Hypothetical protein ATU0119 OR AGR_C_187
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VNG0025H.
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Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
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01-MAR-2001
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01-MAR-2001
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RESULT 45
Q9NMI
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RP SEQUE
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Matches 4; Conserv
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Q9NMI7;
01-OCT-2000
01-OCT-2000
01-OCT-2000
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 9.8 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;

"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";

Science 294.2323-2328(2001).
                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
STRAIN-FRIEDLIN;
Murphy L., Quail M., Harris
Submitted (JUL-2000) to the
EMBL; AL160493; CAB97723.1;
                                                                                                                                                                                                                                                                                      Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID-5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tume C58.";
Science 294:2317-2323(2001).
                                                                                                                                                                   Hypothetical protein.
NON_TER 89 89
SEQUENCE 89 AA; 9751 MW;
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nes 4; Conserv
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             2003, 11:22:00
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                                                                                                                                                                      BD4B82F20965A000 CRC64;
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Pred. No. 1e+03;
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Copyright (c) 1993 - 2003 Compu
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AAW38119
AAE01065
AAY49212
ABB39349
AAM60026
AAM72626
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ABG42450
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                                                       Sorbitol dehydroge
"Peptide 3" consis
G-CSF agonist mAbl
PPPPY motif contai
Horse colostrum-as
Seq ID No: 6 of US
Peptide #6855 enco
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                 Human brain expres
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19	22	22	22	22	22	22	23	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	20	23	22	22	22	22	22	22	22	22
AAW62372	4	AAB90383	AAB90304	AAB90303	AAB90302	AAB90301	ABP09824	AAB90300	AAB90299	AAB90298	AAG78507	AAB90297	AAB90296	AAB90295	AAB90294	AAB90293	AAB90292	AAB90291	AAB90290	AAB90289	AAB90288	AAB90287	AAB90286	AAB90285	AAY12228	ABG37890	AAM03882	AAM28645	1	m	596	2056	B3513	ABB29961
Antithrombotic pep	Human SAA internal	SAA	-	SAA		SAA c	Human ORFX protein	Human SAA carboxy		Human SAA carboxy	seru	SAA	SAA		SAA	SAA car	5' EST s	peptide	#2564	#2682	de #25	bone n	rain ex	#2560	tide #2645	Peptide #2612 enco								

ALIGNMENTS

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RESULT 1
AAB35994
WPI; 2000-687351/67.
                                       Choi E,
                                                               (CHOI/) CHOI E. (RHEE/) RHEE S.
                                                                                                                        02-NOV-2000.
                                                                                                                                       WO200065066-A1
                                                                                                                                                       Gluconobacter oxydans.
                                                                                                                                                                     Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol; L-sorbose production; 2-keto-L-gulonic acid.
                                                                                                                                                                                               Sorbitol dehydrogenase subunit 2 internal peptide.
                                                                                                                                                                                                                 01-MAR-2001
                                                                                                                                                                                                                                AAB35994;
                                                                                                                                                                                                                                               AAB35994 standard; Protein; 7 AA
                                                       (LEEE/)
                                                                                       23-APR-1999;
                                                                                                       23-APR-1999;
                                                      LEE E.
                                      Rhee S,
                                                                                                                                                                                                                (first entry)
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Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule isolated from Gluconobacter suboxydans useful for the fermentative

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                                                                                          RESULT 2
AAP82045
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Best Local Similarity
                                                                                                         An antibody capable of recognising Amyloid A and this peptide
but which does not react with other specified peptides
(see AAP82046-9) is useful for detection of secondary amyloidosis
                                                                                         Sequence
                                                                                                                                                                                  Anti-amyloid-A protein monoclonal antibody used esp for detection of sec amyloidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to an isolated membrane-bound sorbitol dehydrogenase (SDH) from Gluconobacter oxydans. The invention includes polynucleotides (AAC83153 - AAC83154) encoding the 3 subunits of SDH (AAB35987 - AAB35989). Also included in the invention are two polynucleotide sequences AAC83156 and AAC83157 which contain the subunit coding regions. The sorbitol dehydrogenase polynucleotide sequences are useful for producing L-sorbose from D-sorbitol and for increasing the production of 2-keto-L-gulonic acid by transforming a host cell, sepecially Gluconobacter with the DNA and selecting the transformed host cell. The present sequence represents the SDH subunit 2 internal
                                                                                                                                                             Claim 2; Page 649;
                                                                                                                                                                                                                      WPI; 1988-094820/14.
                                                                                                                                                                                                                                                                                                                                      JP63044895-A.
                                                                                                                                                                                                                                                                                                                                                              synthetic
                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO
                                                                                                                                                                                                                                                                   13-AUG-1986;
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                                                                                                                                                                                                                                                                                                                                                                              Amyloid A protein; secondary amyloidosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 2-keto-L-gulonic acid and L-sorbose from D-sorbitol
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      consisting of residues 37-47 of amyloid A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                          Ã,
                                                                                                                                                                                                                                                                   86JP-0189810
                                                                                                                                                                                                                                                                                        86JP-0189810.
                                                                                                                                                          6pp;
                                                                                                                                                                                                                                            KOGYO
                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                          Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                    Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 21;
Pred. No. 7.8e+05;
); Mismatches 0;
                                         Mismatches
                                                               DB
                                                                                                                                                                                                                                                                                                                                                                              anti-amyloid A antibody.
                                                                9;
                                         0,
                                                               Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                       Gaps
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                                       0
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RESULT 3
AAY32231
ID AAY3
XX AAY3
AC CAAY3
AC AAY3
AC AAY3
AC CAAY3
AC AAY3
AC CAAY3
AC CAAY
                                                                                                                                                                                                                                                                                                                                                  RESULT 4
AAW38119
           Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conser
Peptide recognition unit; WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; YAP protein; dystrophin; epithelial sodium channel protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents complementarity determining region 3 (CDR3) of the heavy chain variable region of murine monoclonal antibody mAbi74-74-11. This antibody is an example of an agonist molecule that specifically binds to or interacts with human granulocyte colony stimulating factor (G-CSF) receptor to stimulate cell proliferation and differentiation, especially by dimerising the receptor or activating phosphorylation of kinases associated with the receptor. Agonist antibodies can be used to stimulate proliferation of G-CSF-dependent cells, e.g. to differentiate leading to a repopulation of neutrophilic granulocyte lineage cells, especially to treat neutropenia (claimed). They can also be used to detect human G-CSF receptor immunologically.
                                                                                                                                        PPPPY motif containing peptide ENaC-beta.
                                                                                                                                                                                                                                                               AAW38119;
                                                                                                                                                                                                                                                                                                              AAW38119 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of neutropenia by stimulating proliferation of neutrophilic cell lineage progenitors \, - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Page 30; 64pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ni B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-CSF agonist mAb174-74-11 heavy chain variable region CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TANO-) TANOX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9955735-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody; agonist; screehing; neutropenia; therapy; complementarity determining region; CDR; mAb174-74-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Granulocyte colony stimulating factor receptor; G-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY32231 standard; Peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-052805/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sun BNC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0083575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US09466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sun CRY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DВ
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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В
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                                                                                                                                               AAE01065
                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides AAW38115-28 are derived from epithelial sodium channel alpha (ENAC-alpha), beta (ENAC-beta) and gamma (ENAC-gamma) proteins. The peptides contain pPPDY-like motifs, which are found in the prolline rich regions of WBP-1 and WBP-2 proteins. Peptides containing this residue bind to the YAP WW domain, but not the WW domain from dystrophin or to a panel of SH3 domains. Peptides AAW38115-28 were biotinylated and complexed with alkaline streptavidin, and used in a cross affinity mapping experiment. They were tested for their ability to bind to the 3 individual novel WW domains of WWP4 (AAW36797), which were expressed as glutathione-S-transferase expression proteins. The present peptide binds to some of the WW domains of the WWP4 protein. The wW domain is a small functional domain. Its name is derived from the observation that two tryptophan residues, one in the amino terminal portion of the WW
                                                                                                                                                                                                                                                                                                                                                                    domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling and growth regulation or the organisation of the cytoskeleton. Polypeptides containing a WW domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are useful in targetted drug selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-503234/46
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(UYNC-) UNIV NORTH C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09737223-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
Horse; colostrum; serum amyloid A; SAA; antibacterial; antidiarrhoeic;
                             Horse colostrum-associated serum amyloid A (SAA) peptide #3
                                                               17-JUL-2001
                                                                                              AAE01065
                                                                                                                           AAE01065 standard;
                                                                                                                                                                                                            7
                                                                                                                                                                                                                                          1 NYDA 4
                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                           NYDA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.3;
                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                         13 AA;
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 24B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NORTH CAROLINA
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0630916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US05547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "PPPPY motif"
                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pirozzi
                                                                                                                              13
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                         Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç,
                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                      Length 13;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                          0;
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RESULT 6 AAY49212

AAY49212 standard;

peptide;

19

밁 QΨ

N NYDA 5

0;

07-FEB-2000

(first entry)

Seq ID No:

6 of US5977316

meuropiastoma; glioma; soft tissue carcinoma; tumor-associated antigen.

Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;

US5977316-A Unidentified

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Query Match
Best Local
                                                  Matches
                                                                                                                                                                                                                                                 The patent discloses novel colostrum-associated Serum Amyloid A (SAA) from mammals. SAAs are small apolipoproteins that accumulate and associate rapidly with high-density lipoprotein 3 (HDL3) during the acute phase of inflammatory response. They are characterised by the TFLK motif in the N-terminal region which has the ability to stimulate mucin 3 (MUC3) production. Colostrum associated SAAs are used to prevent or treat infectious diseases associated with enteric pathogens (particularly Escherichia coli) such as traveller's diarrhoea, infant diarrhoea, necrotising entercoolitis (NEC), urinary tract infections, and infectious diarrhoea in herd animals. They are used to prevent dysentery and other infectious diseases particularly more the military.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1999; 99US-0425679
14-JUL-2000; 2000US-0218482
17-JUL-2000; 2000US-0218611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein; inflammatory response; mucin 3; MUC3; therapy; Escherichia coli infection; traveller's diarrhoea; infant diarrhoea; necrotising enterocolitis; NEC; urinary tract infection; dysentery; infectious diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-308640/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McDonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200131006-A2
                                                                                                                                                       Sequence
                                                                                                                                                                                                       The present sequence peptide from horse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New colostrum-associated serum amyloid A protein induces mucin production in epithelial cells and is useful to prevent and treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-2000; 2000WO-US29065
                                                                          Local
1 NYDA 4
                                               Similarity 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogen infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 20; 81pp; English.
                                                                                                                                                       13
                                                     Conservative
                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weber A,
                                                                       100.0%;
                                                                                                                                                                                                                                 is colostrum-associated serum amyloid A (SAA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mack DR,
                                                  0,
                                                                          Pred. No.
                                                                                                     Score 23;
                                                     Mismatches
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                                                                          45;
                                                                                                     DB
                                                                                                     22;
                                                  0,
                                                                                               Length 13;
                                                     Indels
                                                  0;
                                                  Gaps
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RESULT 7
ABB39349
ID ABB3
XX ABB3
AC ABB3
XX ABB3
XX Pept
XX Pept
XX Huma
XX Homc
XX Homc
XX 90-1
PR 04-1
PR 26-1
PR 23-1
PR 03-1
PR 04-1
PR 03-1
PR 04-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a monoclonal antibody (MAb) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAb 1A7 has defined light and heavy chain variable region sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2 -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. Sequences MAY49212-216 represent fragments used for comparison with the light chain
            Penn SG
                                                                              21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                  WO200157277-A2
                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                      Human; foetal liver;
                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                            04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                              ABB39349 standard; Peptide; 28 AA
                                                                                                                                                                                                                                                                                                                                                                       ABB39349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection treatment of cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-619711/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NYDA 4
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                                     MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region of MAb
            Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chatterjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                              2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                           2001WO-US00669
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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            DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74pp;
                                                                                                                                                                                                                                                                                    gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
         Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SK,
                                                                                                                                                                                                                                                                                                               bу
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                                                                                                                                                                                                                                                                                                           human foetal liver single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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           Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23;
Pred. No.
           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X
                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
                                                                                                                                                                                                                                                                                   nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                            exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 8
AAM60026
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Best Local S
Matches 4
                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exonucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                            WPI; 2001-483446/52
                                                                                                              Penn
                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                                                              WO200157275-A2
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded
                                                                                                                                                                                                                                                                                                                                                                           AAM60026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                   epilepsy; cancer.
                                                                                                                                                                                                                                                                                                           microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                             AAM60026 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human [fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     measuring human gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NYDA 10
                                                                                                              SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                    brain expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conserv
                                                                                                                               MOLECULAR DYNAMICS INC.
                                                                                                             Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                   2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IJ
                                                                                                            DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO 31984; 639pp + sequence
                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                          exon; gen
s disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to a single
                                                                                                                                                                                                                                                                                                                                                                                             28 AA.
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                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                             Rank | DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                         multiple sclerosis; so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                     protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe for from human
                                                                                                                                                                                                                                                                                                         s; probe;
schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                      SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                      NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                       32131
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the hum brain. They can be used to measure gene expression in brain cell sam which may enable the diagnosis and improved treatment of nervous sys

improved

brain cell samples

system human sxample

4;

SEQ ID NO:

32131; 650pp + Sequence Listing; English

exon nucleic

acid probes

for analyzing gene expression

in

human

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RESULT 9
AAM72626
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                                          Query Match
Best Local S
Matches 4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0020456.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234635.
04-OCT-2000; 2000GB-0024263.
                                                                                                        probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                     Sequence
                                                                                                                                                                The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                              WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; bone marrow expressed exon; gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM72626;
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                                                                                                                                                                                                                                                                                         (MOLE-)
                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                    1 NYDA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes
NYDA 10
                                                                                                                                                                                                            genome-derived single exon nucleic acid probes useful
zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone marrow expressed probe encoded protein
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                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the
                                                                                     28
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                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.
                                                                                     A,
                                                                                                                                                                                       IJ
                                                                                                                                                                                                                                                                    DK,
                                                                                                                                                                                       NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia; lymphoma; myeloma.
                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                      32932;
                                                                                                                                                                                                                                                                    Chen
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                                                                                                                                                                                     658pp + Sequence Listing;
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Pred. No.
                                                     Score 23; DB 22
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                    Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1e+02;
                                                               22;
                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                              Length 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probe;
                                        Gaps
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RESULT 10
ABG42450
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Nlemann-Pick disease; tubercous sclerosis; Gaucher's disease; Nlemann-Pick disease; pulmonary haemosiderosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peptide encoded by genome-derived single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG42450 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                       (MOLE-)
                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ciliary dyskinesis; pulmonary hypertension; membrane disease.
                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                   2000US-180312P.
2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                          2000GB-0024263
                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID 32115
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Claim 27; SEQ ID No 32115; 634pp; English.

CC probes: Also included are a microarray comprising the novel set of probes; he novel set of probes which hybridise at high stringency to a concleic acid expressed in the human lung; measuring gene expression in a cc sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung manal lung (comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung manal lung (comprising can be expression). The array is dentifying exons in a eukaryotic genome, comprising (c) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably confine the least one elements of detectably confine expression of inthe above mentioned microarray; assigning exons to a single exon probe, having a fragment identifying exons from genomic sequence by the method confirming (a) identifying exons from genomic sequence by the method conversion of the exons in the expression of each of the exons in several confirming a probe with the exon, where a common pattern of confirming a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one confirming a probe with the specification, or encoded by the method confirming a probe with the specification, or encoded by the method confirming a probe with the specification, or encoded by the method confirming a probe with the specification or encoded by the method confirming a probe with the specification or encoded by the method confirming a probe with the probes are used for gene of 12011 sequences, probes/open reading The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 frames (ORF). for specification, or encoded by the probes are used for gene particularly of

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RESULT 11
ABB29961
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Best Local S
Matches 4
                  The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part
                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                        WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmon fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary disease (ILD), familial idiopathic pulmonary disease (ILD), familial idiopathic pulmonary disease, hermansky-Pudlak syndrome, sarcoidosis, pulmonary disease, hermansky-Pudlak syndrome, hermansky-Pudlak
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such as asthma,
                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #2612 encoded by breast cell single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                 for measuring
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                                                                                                                                                                                                           comprises number c
                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                     Hanzel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                   DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single exon probe; gene expression; breast;
       of.
                                                                                                                                                              12929;
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                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                                                                                                         e expression in of single exon
                                                                                                                                                                                                                            set of single exon nucleic acid probes, expression in sample derived from human
  breast, and microarray.
                                                                                                                                                                                                                                                                                                                                                   Į.
                                                                                                                                                          327pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                   Rank DR;
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                                                                                                                                                              sequence
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                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                          listing;
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                                                                                                                                                                                                         probes
                                                                                                                                                            English
                                                                                                                                                                                                                                 numan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pulmonary
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RESULT 12
ABB35139
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Best Local
                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exonucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agents on cells. The microarray of this invention presents a rar greaters to cells. The microarray of this invention presents a rar greatersty of probes for measuring gene expression, with far less big than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                            Claim
                                                                                                                                                                      analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical
printed specification, but was obtained
from WIPO at ftp.wipo.int/pub/published
                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #2645 encoded by human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2002
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                           Note: The sequence data
                                                                                                                                                                                                                                                                       (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB35139 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      verifying the expression of regions of genomic DNA predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 NYDA 33
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                                                                                                                                                                                                                 2001-483447/52
                                                                                                                                                                                                                                             SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                            27;
                                                                                                                                                                                       genome-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             foetal
                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                            SEQ
                                                                                                                                                                      gene
                                                                                                                                                                                                                                           Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA,
                                                                                                                                            ID NO 27774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                      expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The microarray of this invention presents a far greater bes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                    single exon
                                                                                                                                                                                                                                           Chen W,
                           for this patent did not form part of
                                                                                                                                                                      'n
                                                                                                                                         639pp + sequence listing; English
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                                                                                                                                                                     exon nucleic
human fetal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23;
                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
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 _pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4e+02;
                in electronic
                                                                                                                                                                      acid probes useful for liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       he method is suitable for from genomic sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                format
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                                                    Query Match
Best Local S
Matches 4
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023459.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format directly from WIPO at for with published et accuracy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               congenital heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB20561 standard; Protein; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein #2560 encoded by probe for measuring heart cell gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2002
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                                                    Local Similarity
nes 4; Conserv
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                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36
                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22331; 530pp; English.
                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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Pred. No. 1.4e+02;
                                                                           Score 23; DB 22;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                      Mismatches
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                                                                                                     Length 36;
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                                                    Indels
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6.
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                                                 Gaps
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RESULT 15
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                                                                                                                                                              Matches
                                                                                                                                                                                  Query Match
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                     06-NOV-2001
                                                              AAM68335 standard;
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                          epilepsy and cancers. The present sequence is a protein encoded the probes of the invention.
                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid brains -
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray; Alzheimer's
epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM55966;
                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM55966 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 NYDA
                                                                                                                                                                        Local Similarity
                                                                                                                                        1 NYDA 4
                                                                                                                     NYDA
                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC
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u
                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                         36
                                                                                                                                                              100.0%;
ilarity 100.0%;
Conservative (
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2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-0234687.
2000US-02346359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00667
                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                         Ā
                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                28071; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                 probes
                                                                36
                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36
                                                                                                                                                                        Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe encoded protein
                                                                                                                                                                                                                                                                                                                                                                                            DR;
                                                                                                                                                                         1.4e+02;
                                                                                                                                                                                    DB 22;
                                                                                                                                                                                  Length 36;
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28071
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Human bone marrow expressed probe encoded protein SEQ ID

NO:

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RESULT 16
AAM16152
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                                                                                                                                                                                                                                                                                                                Matches
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Best Local :
 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                              09-AUG-2001.
                                                                               WO200157278-A2
                                                                                                                          cervical
                                                                                                                              Probe; human; microarray; gene expression; cervical epithelial cell;
                                          30-JAN-2001;
                                                                                                     Homo sapiens
                                                                                                                                                      Peptide #2586 encoded by
                                                                                                                                                                             12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                   AAM16152 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bone marrow expressed en microarray; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157276-A2
                                                                                                                                                                                                                                                                        30 NYDA
                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                          1 NYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful
zing gene expression in human bone marrow -
                                                                                                                          cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:
2000US-0180312.
2000US-0207456.
2000US-0608408.
                                         2001WO-US00670
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DK,
                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                             100.0%; S
100.0%; F
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            28641; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                       probe
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                                                                                                                                                                                                                    36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                      Score 23; DB 22;
Pred. No. 1.4e+02;
                                                                                                                                                 for measuring cervical gene expression
                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphoma; myeloma
                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                               Length 36;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                            0;
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RESULT 17
AAM28645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                   04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234599.
04-OCT-2000; 2000GB-0024263.
                       Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                            (MOLE-)
                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                WO200157272-A2
                                                                                                                                                                                                                                                               genetic disorder.
                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; lantenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microraarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                              Peptide #2682 encoded by probe for
                                                                                                                                                                                                                                                                                                                          17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                 AAM28645;
                                                                                                                                                                                                                                                                                                                                                                     AAM28645 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                 30 NYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                       SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                            MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                      Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative C
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2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID No 20978; 487pp; English.
                                                                                                                                                                                                                                                                                                                       entry)
                      Chen
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                      Œ,
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                                                                                                                                                                                                                                                                                                                                                                      36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DE Pred. No. 1.4); Mismatches
                      Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                                                                                             measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
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SENPS

WPI; 2001-488897/53.

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Matches
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Best Local Similarity
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26-MAY-2000;
30-JUN-2000;
The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing
                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                         Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM03882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM03882 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                     SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYDA 33
                                                                                                                                                                                                                                                                                               2001-476286/51
                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                        single exon nucleic acid
human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS
                                                                                                                                                                                                SEQ ID No 12622; 322pp; English
                                                                                                                                                                                                                                                                                                                                     Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression
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2000US-0207456.

2000US-060840B.

2000US-0632366.

2000US-0234687.

2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US00661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease; proliferative breast disease; non-carcinoma tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                     DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bу
                                                                                                                                                                                                                                                                                                                                     Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 22;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                         probe used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         placenta
                                                                                                                                                                                                                                                         measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful
                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression
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                                                                                                                                                                                                                                                         expression
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RESULT 19
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Matches
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-tick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000;
03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; single exon probe; asthma; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide encoded by genome-derived single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast disease and non-carcinoma tumours.
Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                        Claim
                                                                                                                                                                                 measure gene expression in human lung
                                                                                                                                                                                               Spatially-addressable set of single exon nucleic acid probes,
                                                                                                                                                                                                                                                                                 (MOLE-)
                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyaline membrane
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                                                                                                                                                                                                                                                                                 MOLECULAR DYNAMICS INC
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2000US-0632366.
2000US-234687P.
2000US-236359P.
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cc mRNA, and (b) measuring the label detectably bound to each probe of cc (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon cc tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of cc expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the exonession analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary surrogeners, reproduces sclerosis, Gaucher's disease, cc unimonary dysplasia, primary ciliary dyskinesis, garcoidosis, pulmonary histiocytosis, lumporary hypertension and hyaline membrane disease. The present sequence is a peptide/protein context the sequence data for this patent did not form part of the winn intromation, but was obtained in electronic from and not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haematostatichrombolytic; anti-inflammatory; tumour inhibition.
      Duclert
                                                                  (GEST ) GENSET
                                                                                                                             01-AUG-1997;
                                                                                                                                                                                        31-JUL-1998;
                                                                                                                                                                                                                                                          11-FEB-1999
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Dumas Milne Edwards
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                                                                                                                             97US-0905134
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100.0%; P
ative 0;
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Pred. No. 1.4e+02;
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Lacroix
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New serum amyloid A and formyl peptide receptor variant complex and its

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RESULT 21
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Best Local S
Matches 4
                            WPI; 2001-211457/21
                                                                                                                                                                                                                                                                        antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; ca immune system disorder; amyloidosis; inflammation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into
                                                        Wang J,
                                                                                                                                            22-SEP-1999;
                                                                                                                                                                                                                                                                                                           FPRL1;
                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                           29-MAR-2001.
                                                                                                                                                                                                     W0200121188-A1
                                                                                                                                                                                                                                                                                                                                                   Human SAA carboxy truncation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY01602 and AAX11994 to AAX12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB90285 standard; Protein; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding human secreted proteins - obtained cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
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                                                                                                                                                                                                                                                               rejection;
                                                                                                                                                                                                                                                                                                        immunomodulatory; antiinflammatory;
                                                                                                                                                                                                                                                                                                                         serum amyloid A; SAA; human
                                                                                     SD
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                                                      Oppenheim JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
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                                                                                                                                            99WO-US21770
                                                                                    HEALTH & HUMAN
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Pred. No.
                                                                                 SERVICES
                                                    Gong W,
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                                                                                                                                                                                                                                                                                                   formyl peptide receptor variant;
mmatory; antimicrobial; antiarthritic;
                                                    Gao J,
                                                                                                                                                                                                                                                                                           SAA/FPRL1 complex; cancer;
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                                                    Murphy
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                    The present sequence is a fragment of human serum amyloid A (SAA). Invention relates to the discovery that SAA is a ligand for FPRLI (formyl peptide receptor variant). A complex has been isolated that comprises a peptide agent with a sequence corresponding to SAA, or conservative variant or functional fragment, bound to FPRLI. Modula of the SAA/FPRLI complex are useful for treating immune system
                                                                                                                                                                                                                                                                                                       New serum amyloid A and formyl peptide receptor variant complex and its modulators, useful for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested for their ability to modulate assembly of the SAA/FPRL1 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
immune system disorder; amyloidosis; inflammation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                          Disclosure; Page 15; 141pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arthritis; atherosclerosis.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERVICES
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Best Local
                                                                       The present sequence is a fragment of human serum amyloid A (SAA). The invention relates to the discovery that SAA is a ligand for FPRLI (human formyl peptide receptor variant). A complex has been isolated that comprises a peptide agent with a sequence corresponding to SAA, or its conservative variant or functional fragment, bound to FPRLI. Modulators of the SAA/FPRLI complex are useful for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested for their ability to modulate assembly of the SAA/FPRLI complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic; antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer; immune system disorder; amyloidosis; inflammation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                     Disclosure;
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                                                                                                                                                                                                                                        serum amyloid A and formyl peptide receptor variant complex and ulators, useful for treating immune system disorders, amyloidosis lammation, infection, organ rejection, arthritis, atherosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   serum amyloid A; SAA;
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               Similarity
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                                                                                                                                                                                                                                                                                                                    Oppenheim JJ,
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100.0%; ilarity 100.0%; Conservative
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             Score 23;
Pred. No.
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AAB90289
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KW Huma
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AAB90288
ID AAB90
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Best Local
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                                                                                           Human SAA carboxy truncation,
                                                                                                                                                       01-JUN-2001
                                                                                                                                                                                                                AAB90289;
                                                                                                                                                                                                                                                          AAB90289 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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serum amyloid A; SAA; human formyl peptide receptor variant; immunomodulatory; antiinflammatory; antimicrobial; antiarthr
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Pred. No. 1.9
); Mismatches
                                                                                        SEQ ID NO: 47.
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  antiarthritic;
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RESULT 26
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22-SEP-1999;
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                             22-SEP-1999;
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                                                                                                                        Homo sapiens.
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immune system disorder; amyloidosis; inflamm
organ rejection; arthritis; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                            42 NYDA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NYDA 4
                                                                                                                                                       rejection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 AA;
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                                                                                                                                                                                                                                                                              (first entry)
                            99WO-US21770.
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                                                                                                                                                       arthritis;
                                                                                                                                                                                                                                                                                                                                              Protein;
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                                                                                                                                                  atherosclerosis.
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                                                                                                                                                                                                                                               SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 22;
Pred. No. 1.9e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ve; SAA/FPRL1 complex; cancer;
inflammation; infection;
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                     Human; serum amyloid A; SAA; human formyl peptide receptor variant; FPRLI; immunomodulatory; anttinflammatory; antincrobial; antiarthritic; antiatherosclerotic; immunosuppressive; SAA/FPRLI complex; cancer; immune system disorder; amyloidosis; inflammation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested for their ability to modulate assembly of the SAA/FPRL1 complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
                                                                                                                                                                                                                                                                                                                                                                    Human SAA carboxy truncation,
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB90291;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB90291 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New serum amyloid A and formyl peptide receptor variant complex and its modulators, useful for treating immune system disorders, amyloidosis,
                                                                                                                                                                                       22-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001
                                  inflammation,
                                                  modulators,
                                                                                                            Wang J,
                                                                                                                                     (USSH)
                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation,
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                               serum amyloid A and formyl peptide receptor variant complex and its ulators, useful for treating immune system disorders, amyloidosis, lammation, infection, organ rejection, arthritis, atherosclerosis
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                                                                                                                                                                                                                                                                                          rejection;
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4; Conserv
                                                                                                            Oppenheim JJ,
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                           infection,
                                                                                                                                                              99WO-US21770.
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                                                                                                                                     HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                          arthritis;
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100.0%; P
ative 0;
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                                                                                                                                                                                                                                                                                          atherosclerosis.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO: 49.
                                                                                                            Gong W,
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thes 0;
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                                                                                                            Murphy PM;
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Disclosure; Page 15; 141pp; English

The present sequence is a fragment of human serum amyloid A (SAA). The invention relates to the discovery that SAA is a ligand for FPRL1 (human formyl peptide receptor variant). A complex has been isolated that comprises a peptide agent with a sequence corresponding to SAA, or its conservative variant or functional fragment, bound to FPRL1. Modulators of the SAA/FPRL1 complex are useful for treating immune system

Disclosure; Page 15; 141pp; English.

inflammation,

infection,

organ

rejection,

arthritis, atherosclerosis

New serum amyloid A and formyl peptide receptor variant complex and its modulators, useful for treating immune system disorders, amyloidosis,

Wang

Oppenheim JJ,

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Murphy

WPI;

2001-211457/21.

disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia. Fragments of SAA were t for their ability to modulate assembly of the SAA/FPRL1 complex.

fragments of the SAA/FPRL1

tested

Sequence

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AAB90292
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Best Local :
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                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                            22-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                     therosclerotic; immunosuppressive; system disorder; amyloidosis; in rejection; arthritis; atherosclero
                                                                                                                                                                                                                                                                                                                                                                                                                                   serum amyloid A; SAA;
                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                            ry; antimicrobial; antiarthritic;
SAA/FPRL1 complex; cancer;
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AAB90293
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Best Local Similarity
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Best Local Similarity
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AAB90294 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPRII; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic; antiatherosclerotic; immunosuppressive; SAA/FPRII complex; cancer; immune system disorder; amyloidosis; inflammation; infection; organ rejection; arthritis; atherosclerosis.
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                           New serum amyloid A and formyl peptide receptor variant complex and its modulators, useful for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis
                                                                                                                                                                                                                                                                                                            Disclosure; Page 15; 141pp; English.
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                                                                                                                                                                                                                                                                                                                                      and neoplasia
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                                                                                                              Conservative
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100.0%; F
tive 0;
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54 AA
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                                                                                                                       Score 23; DB 22;
Pred. No. 2.1e+02;
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Pred. No.
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2e+02;
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Matches
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Best Local
                                                    antiatherosclerotic; immunosuppressive;
immune system disorder; amyloidosis; inf
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                                                                                                                                                                                                                         AAB90295;
                                                                                                                                                                                                                                                         AAB90295 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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and neoplasia –
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH)
                                                                                                                                                                                                                                                                                                                                                  42 NYDA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                     1 NYDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the SAA/FPRL1 complex are useful for treating immune system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-211457/21.
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                                       rejection; arthritis;
                                                                                                                                              SAA carboxy truncation,
                                                                                    serum amyloid A; SAA; human formyl peptide receptor variant;
immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serum amyloid A; SAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oppenheim JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 16; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amyloid A; SAA; human formyl peptide receptor variant; modulatory; antiniflammatory; antimicrobial; antiarthritic; erotic; immunosuppressive; SAA/FPRL1 complex; cancer; disorder; amyloidosis; inflammation; infection; on; arthritis; atherosclerosis.
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                                                                                                                                              SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 22;
Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                      inflammation;
                                                                       SAA/FPRL1 complex; cancer;
                                                                                                                                              53.
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QY밁